

C	27	50	4.9	14809	1	PCT-US02-09188-510	Sequence 914, App
C	28	50	4.9	14809	1	PCT-US02-09370-950	Sequence 950, App
C	29	50	4.9	14809	6	US-10-105-299-6325	Sequence 6325, App
C	30	50	4.9	46983	6	US-10-105-299-13935	Sequence 13935, App
C	31	49.4	4.8	375	5	US-09-789-189-1457	Sequence 1457, App
C	32	49.4	4.8	755	6	US-10-027-633-128190	Sequence 128190, App
C	33	49.2	4.8	1127	6	US-10-027-633-119520	Sequence 119520, App
C	34	48.8	4.8	843	6	US-10-027-633-7034	Sequence 7034, App
C	35	48.4	4.7	529	5	US-09-789-189-835	Sequence 835, App
C	36	48.4	4.7	628	6	US-10-027-633-233402	Sequence 233402, App
C	37	48.4	4.7	628	6	US-10-027-633-233403	Sequence 233403, App
C	38	47.8	4.7	628	6	US-10-027-633-211511	Sequence 211511, App
C	39	47.8	4.7	658	6	US-10-027-633-211511	Sequence 211511, App
C	40	47.8	4.7	858	6	US-10-027-633-27031	Sequence 27031, App
C	41	47.6	4.7	534	6	US-10-027-633-242384	Sequence 242384, App
C	42	47.6	4.7	534	6	US-10-027-633-242385	Sequence 242385, App
C	43	47.6	4.7	534	6	US-10-027-633-242386	Sequence 242386, App
C	44	47.6	4.7	628	6	US-10-027-633-113152	Sequence 113152, App
C	45	47.6	4.7	3233	5	US-09-919-002-2106	Sequence 2106, App

Query Match	8.0%;	Score 81.8;	DB 6;	Length 13859;
Best Local Similarity	44.9%;	Pred. No. 7.4e-05;		
Matches 349;	Conservative	0;	Mismatches 427;	Indels 1;
				Gaps 1

QY	107	AATTAATTGATCAAAATTTTCAGTCTCCACCACTTCACATCATCGAGAATTTTTATAC	160
Db	7696	ATTATAATTAATCATTATATATAAATGTATATCCCAATAATATATATATATTTTATTAC	76
QY	167	TTAACAATTTGAACACATCCMAACATTAATGAAATTTTTTAATGATCTTAAATTTATG	228
Db	7636	ATTAGAAATTTTATATATACATATATCTATATTAACATCTGTATATATATATATATAT	75
QY	227	ATGANGTATATATATACCAAAATTTGATGCTATGATTTTGACTCAATTCATGGAAATTA	288
Db	7576	GTTACATATATTATATATATATATATATATATATACATGCTTTATACATATATATAATCA	75
QY	287	CAAAATTTTGTAAACGAACAACAGATTTTATATGATATTAATGTAATCTGTATACGA	348
Db	7516	TATAAATTTATTAATAATTAATAATACCAAATPATATAAATATATATGAAATATTAATTA	74
QY	347	ATCATATATACACTGCTATATGAAATTTGAGAAAAAGATATCAAATTTATGTTTAAATCAA	408
Db	7456	TAAATATATATGTAATAATATATATTAATAATTCATATAAGTAAATATTTTAAAAAACCAATATA	738
QY	407	TGAGTTCAGSACTGTAATTTATTCATCCACAAGSATAATTCATGCTGATTTAAACCCA	468
Db	7396	AAATATATATGCANTATATATATTAATAAATTTACCTTATATATTTATATATATATTTATT	738
QY	467	GTAATATTTTCTTTGCCCGGAGTATATTAACACACCGATTAATTTGAGATTTTGATATT	528

[illegible]

	Query Match	Similarity	6.8%	Score 69.4	DB 6	Length 20420
	Best Local	Similarity	44.1%	Pred. No. 0.0067		
	Matches	340	Conservative	0	Mismatches 426	Indels 5
					Gaps	1
QY	142	TCGATCCATCGAGGAATTTTATCTACTTAACCTTGAACCCATCCACATTAATTGAA	201			
Db	4082	TCAGCGAGCCATATATATGATATATATATATATATATGAAAAATATATATATATATA	4141			
QY	202	TATTTTAATGATCTTAAATTTTATGATGATGTTATTTATGTCACCAATTTGATCGTTAT	261			
Db	4142	TATATGAAAAATGAA	4201			

OY	262	GATTGGCGTAATTTGATTGAAATTTACAAAATATGTGAAGCAACAACCAGTATTTAT	321
Dd	4202	aatacacaataatatacaataacataaacataatatatacatataaatatatt-----	4257
OY	322	GGTATTATGGTAATCTTGTTACTAATCATATATCACCTTGCTAATGAATTCGACAAAA	381
Dd	4258	-aigaaatacataataatataatataatataatataatgaaaatafatatgatgaanaa	4316
OY	382	CATATCAAATTAGTITTAATAATCANTGAGCTGCAGACTTGAATTTATTCATTCCACAGG	441
Dd	4317	tataTgaaaaataataataataataataTaTgaaaaataataataataataataTg	4376
OY	442	AATAATCATCGTGAATPFAAACCCAGTAATATTTTTCTTGCCCGAGATGATPAACAA	501
Dd	4377	aaatacacataataataataataataTgaaaataataataataataataataTgaaa	4436
OY	502	CCGATVATFGAGATVVTVGVATVTGTTATGATTTTAAACGCCACTMAAGATCACCC	561
Dd	4437	tataataataataataataataTgaaaataataataataataataataataTgaaaata	4496
OY	582	CCATMGCGAATPATATTTGATGTATCAGAGTATTTAAAGCACCGAATVGATTCCT	621
Dd	4437	tataaaataataataataTgaaaataataataataataataataataataataataata	4556
OY	622	GGTATTACTIONTATVGAATPTGAATVTGATVTTTGGCTVTTGGGTATTAATTTTGCATGT	681
Dd	4557	TaaataataataataTgaaaataataataataataataataataataataataataata	4616
OY	662	TTATATTTCAGAAATTTCCAAGTGTTTTAGTCAAGAATGATMAAGATGCTATATAT	741
Dd	4617	tataataTgaaaataataataataataataataataataataataataataataataata	4676
OY	742	TCTCATGTACTGATVATATTTATTPAANAATATTTGAATAATTTGGTACACCCCAT	801
Dd	4677	TatgaaaataataataataataataataTgaaaataataataataataataataataata	4736
OY	802	TTAACGATTTTGAAGATTAATTTTGTGATGAATATPATATPGAAAATCTGCATTTT	861
Dd	4737	tataataTgaaaataataataataataataataataataataataataataataataata	4796
OY	862	AAAAAAAAATTCATTTCAAAAAATATCCFAGAAAAAGNTGGATATATTTATTTTA	912
Dd	4797	ataataaaaaaaaaataataataataataaaaaataataataataataataataata	4847

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RESULT 3
US-10-105-299-12506
; Sequence 12506: Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ. ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO. 12506
; LENGTH: 13859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-12506

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Query Match	Similarity	Score	DB	Length
Best Local	44.4%	Pred No. 0.023		
Matches	416	Conservative	0	Mismatches 500; Indels 20; Gaps 3
QY	73	ATTGATAGCTTAATPACTTACCAGTANGCTTAAATAATGTTGAGGAACTTCAGTCTT	132	
Db	6350	atagataataataactatctatataataataataataataatataatgtaagaattgtaata	6409	
QY	133	CCACGCATCTTCATCCATCGATCGAGAAATTTTAACTTAAAACTTGAACACATCCCAAC	192	

Query Match	Best Local Similarity	Score	DB	Length
Matches 343; Conservative	43.3%;	6.2%;	6;	20420;
	0;	Pred. No. 0.064;		
		Mismatches 448; Indels 1; Gaps 1;		
138	ACATTCATCCATCGAGAAATTTTATACCTTAAACTTTGAAACCAACATCCAAACATAT	197		
4883	AAAAAT	4824		
136	TGAATATTTTAAATGATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT	257		
4823	TAT	4764		
258	TTATGATTTGATCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	317		
4763	ATATTTTAT	4704		
318	TTAT-GGATTTAAATGATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT	376		
4703	AT	4644		
377	AAAAAGATATCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	436		
4663	ATATTTTAT	4584		
437	AAGGATATATTCATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	496		
4583	AT	4524		
497	CACAAACGATTTATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	556		
4523	ATATTTTAT	4464		
557	AACCCCATATGCGCAAT	616		
4463	TTTCAT	4404		
617	TTTCATGATTAACAT	676		
4403	AT	4344		
677	CTGCTTATATATCGAAAAATTTTCAAAAGCTTTTAAAGTCAAAAGATGATTAAGAAAT	736		
4343	AT	4284		
737	ATGATTCATCATGATTAAGATTTTATATATATATATATATATATATATATATATAT	796		
4283	AT	4224		
797	CCAATTTAACTGATTTGAGATGATTTTATATATATATATATATATATATATATAT	856		
4223	TAT	4164		

Db 1164 aattlaataaatacatatlaaaaaagcctaattlaatatattacgtlaataatlaaacaactct 1223
Oy 217 AAAATTTATGATGATGTTATATTA---GTCACCAAAATTGATCGTTATGATTTAGTGCA 273
Db 1224 tatcttaccgttlaactatlaataatlaataatlaataatlaataatlaataatlaataatc 1283
Oy 274 TTGATTTCAAAATTTGTAACAAATGTAACGACGATTTATTTATTTATTTATTTATTTAT 333
Db 1284 taactatataataatlaataatlaataatlaataatlaataatlaataatlaataatlaata 1343
Oy 334 AATCTTGTGTAATCAATATACATTTGCTAATGAAATTTGAGAAAAGATATCAAAATTA 393
Db 1344 atattataataatlaataatlaataatlaataatlaataatlaataatlaataatlaata 1403
Oy 394 TGGTAAATCAATGAGCTTGACAGCTTGATTTATTCATTCACAGGCAATTAATTCATCGT 453
Db 1404 atacaataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1463
Oy 454 GATTTAAACCCAGTAATATTTCTTTGCCCCGAGATATTAACACAGCGATTTATTTGA 513
Db 1464 aataataatcttataatlaataatlaataatlaataatlaataatlaataatlaataat 1518
Oy 514 GATTTGATATTTGTTGTTATTTAAACCTGACCTTAAGATGACCCCTATGGCGAA 573
Db 1519 agtattcaatataatlaataatlaataatlaataatlaataatlaataatlaataatla 1578
Oy 574 TATATTGATGATGATGATGATTTATTTAAAGCAGCAAGATTTGATTTGATTAATTAAT 633
Db 1579 ttataataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1638
Oy 634 TATGATATGAAATTTGATTTGGTCAATTTGGGATTAAT-TTTCAGCTGTTTATATTCGA 692
Db 1639 atataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1698
Oy 693 AAAATTTCAAGTGTTTAGTCAAGATGTAAGATTTGACATTAATGATTTTCAATGTTAG 752
Db 1699 atataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1758
Oy 753 TGATTTATTTATTTAAATCAATATTTGAAATTTGCGACCCCAATTTAACTGATTT 812
Db 1759 atataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1818
Oy 813 TGAGATGAATTTATTTGATGATTAATTAATGAAATTTGCAATTTAAATTTAAATTTCA 872
Db 1819 ataataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1878
Oy 873 TTTACAAAATATCTAGAAAAGATTTGATTTATTTTACCTCGATGCAATGATGATTT 932
Db 1879 aataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1938
Oy 933 AATGAAAGAAATTTTACCAAGATGATTAATGATGATGCAAGTAAGTAAGATTAATCTTAA 992
Db 1939 taataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1998
Oy 993 AGAAATCTTA 1002
Db 1999 ataataagta 2008

RESULT 7
US-10-027-632-113788
; Sequence 113788, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 113788
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113788

Query Match 6.2%; Score 62.8; DB 6; Length 3252;
Best Local Similarity 44.6%; Pred. No. 0.072;
Matches 379; Conservative 0; Mismatches 462; Indels 9; Gaps 3;

Oy 157 ATTTTATTTACTTAAACTTTGAAACCAATCCAAACATTAATTTGATTTTATGATCTT 216
Db 1164 aattlaataaatacatatlaaaaaagcctaattlaatatattacgtlaataatlaaacaactct 1223
Oy 217 AAAATTTATGATGATGTTATATTA---GTCACCAAAATTGATCGTTATGATTTAGTGCA 273
Db 1224 tatcttaccgttlaactatlaataatlaataatlaataatlaataatlaataatlaataatc 1283
Oy 274 TTGATTTCAAAATTTGTAACAAATGTAACGACGATTTATTTATTTATTTATTTATTTAT 333
Db 1284 taactatataataatlaataatlaataatlaataatlaataatlaataatlaataatlaata 1343
Oy 334 AATCTTGTGTAATCAATATACATTTGCTAATGAAATTTGAGAAAAGATATCAAAATTA 393
Db 1344 atattataataatlaataatlaataatlaataatlaataatlaataatlaataatlaata 1403
Oy 394 TGGTAAATCAATGAGCTTGACAGCTTGAAATTTATTCATTCACAGGATTAATTCATGCT 453
Db 1404 atacaataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1463
Oy 454 GATTTAAACCCAGTAATATTTCTTTGCCCCGAGATGATTAACACAGCGATTTATTTGA 513
Db 1464 aataataatcttataatlaataatlaataatlaataatlaataatlaataatlaataat 1518
Oy 514 GATTTGATATTTGTTGTTATTTAAACCTGACCTTAAGATGACCCCTATGGCGAA 573
Db 1519 agtattcaatataatlaataatlaataatlaataatlaataatlaataatlaataatla 1578
Oy 574 TATATTGATGATGATGATTTATTTAAAGCAGCAAGATTTGATTTTGGTATTAATTAAT 633
Db 1579 ttataataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1638
Oy 634 TATGATATGAAATTTGATTTGGTCAATTTGGGATTAAT-TTTCAGCTGTTTATATTCGA 692
Db 1639 atataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1698
Oy 693 AAAATTTCAAGTGTTTAGTCAAGATGTAAGATTTGACATTAATGATTTCAATGTTAG 752
Db 1699 atataataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1758
Oy 753 TGATTTATTTATTTAAATCAATATTTGAAATTTGCGACCCCAATTTAACTGATTT 812
Db 1759 atataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1818
Oy 813 TGAAGATGAATTTATTTGATGATTAATTAATGAAATTTGATTTTAAATTTAAATTTCA 872
Db 1819 ataataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1878
Oy 873 TTTACAAAATATCTAGAAAAGATTTGATTTATTTTACCTCGATGCAATGATGATTT 932
Db 1939 taataataataatlaataatlaataatlaataatlaataatlaataatlaataatla 1998

Db	1866	AACAATATTTATATATATATATATTCACAACCAATATTTATATATATATATTAATA	1807
Qy	789	CGGTAAACCAATTTTACGATTTTGAGATGCAATTTTGTGATGCAATATATATTA	848
Db	1806	CAATATATATTTATATATTTAAATATACAAATTTTATATATATATATTTAAATATCAAT	1747
Qy	849	AAATCGCATTTTAAATAATTCATTTTCAAAAATATCTAGAAAAGATTCGATTTAT	908
Db	1746	ATTATATATTTAT - ATATTTTAAATATACAAATTTTATATATATATATATTAATATAC	1688
Qy	909	TTTAAACCGATGCAATGATGATTTATATGAAAGAAATTTTACCAAGATGATGATAT	966
Db	1687	AAATTTATATATTTATATATATTTATATATACAAATTTTATATATATATATATTAATAT	1630

RESULT 10

US-10-027-632-113787/c

Sequence 113787, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Mang David G.

TIME OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1998-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 113787

LENGTH: 3252

TYPE: DNA

ORGANISM: Human

US-10-027-632-113787

Query Match 5.9%; Score 60.4; DB 6; Length 3252;

Best Local Similarity 46.6%; Pred. No. 0.17;

Matches 446; Conservative 0; Mismatches 491; Indels 21; Gaps

Qy	10	TCAGATTATATATTAACAAGAAATTAATTTACAAATAGTCGATTTCTGATATATATAGC	69
Db	2567	TTAATATCTATATATACCTAATGTAAGATATATATCTATATTTAAAGTATACATTAAG	2508
Qy	70	GCATTCATAGTTTATACTTACCACTGATGCTTAAATAGTTGATGGAAGATTTCACT	129
Db	2307	TATATTAATATAGATATTT - TTAATATACATGTCATTTAAAGTATATGATATATCAATT	2450
Qy	130	CTTCCACACATTCGATTCGATGAGAAATTTTATATCTTAAACCTTTGAAACCAACATCCA	189
Db	2449	GAAATATATTAAT - - - - - ATATTTTAACTTTAACACTTTAAATTTAATATATAATATA	2396
Qy	190	AACTATATTAATTTTATATGATCTTAAATTTATATGATATGTTATATATAGTCACCAAA	249
Db	2395	TACTATAGACTAATATATTTTAAACCTTTTATATATATATATATATATATATATGTTATACCT	2336
Qy	250	TT-GTATCGTTATGATTTGAGTCAATGATATGCAAAATTTGCAAAATATTTGAAACGAACAC	308
Db	2335	TTAAATATATTAAGTATATAATTAATATACACAAATTTTATATCTTATATATATATGAGCTTA	2276

QY	309	ACGATTTATTATGCTGTTTATGTAATCTGTGTAGTATATCAATATTAACCTGGTAATGA	368
Db	2275	ATAATGTTTATAGCTATATATATATTTTAAAGCTGTATGTAACATATGATTAAGTTAATAT	2216
QY	369	AATTGAAGAAAAAGATATCAATTAATGCTTTAAATCAATGAGTTCAGACTTGAATTTAT	428
Db	2215	ATTAAATTTTAT	2158
QY	429	TCATTTCAAGAGGTAATATTCATGCTGATATTAATTAACCCAGTAATATTTCTTGGCCCGGA	488
Db	2157	TAATTCATATATATATATTTTA-----ATATATATACCATATTAATCTTATATTAAGAAGC	2104
QY	489	TGATATATACACACCCATTATTTGGAGATTTTGATATTTGTTATGATTTAAACCTGCCAC	548
Db	2103	TAAATTTAATATATATATACATTAATCTGA--TAAATCTTTATCTTATGTTAACTTCAAT	2047
QY	549	TAAAGATGAACCCCTATGGCGAAATATATATGATGTATCTACAGATATTTATTAAGCAC	608
Db	2046	AAATTAATTAATATATATTAATTAATTAACCTATTAATCTGTTAACTATATATATATAGTTAAC	1987
QY	609	AGAAATGATCTTGCTATTAATCTATATATATATATATATATATATATATATATATATAT	668
Db	1986	ATATTAATAAT	1922
QY	669	AATTTTGACGTGTTTATATATTCAGAAAAATTTTCAAGGTGTTTAGTCAAGATGATAAAGA	728
Db	1926	TATTTAT	1867
QY	729	ATTCATATATATCTCATATGTTAGTGTATATATATATATATATATATATATATATATAT	788
Db	1866	AATCAT	1807
QY	789	CGGTACACCCATTTTAACTGATTTTGAAGATTAATTTTGTGATGAATATATATATGA	848
Db	1806	CAAT	1747
QY	849	AAACTGATATTTTAAATAATTCATTAATCAAAATATATCTGAGAAAGATTTGGCATATAT	908
Db	1746	ATTATATATATATAT--ATATATTTTAATATACAAATTTTATATATATATATATATATAT	1688
QY	909	TTTACCTGATGCAATGATGATTTTATGAAAAGAAATTTTACCAGATCATATAGAT	966
Db	1687	AATATTTAT	1630
RESULT 11			
US-10-027-632-113788/c			
: Sequence 113788, Application US/10027632			
: GENERAL INFORMATION:			
: APPLICANT: Wang, David G.			
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide			
: FILE OF INVENTION: Polymorphisms in the Human Genome			
: FILE REFERENCE: 108827.129			
: CURRENT APPLICATION NUMBER: US/10/027,632			
: CURRENT FILING DATE: 2002-04-30			
: PRIOR APPLICATION NUMBER: US 60/218,006			
: PRIOR FILING DATE: 2000-07-12			
: PRIOR APPLICATION NUMBER: US 60/198,676			
: PRIOR FILING DATE: 2000-04-20			
: PRIOR APPLICATION NUMBER: US 60/193,483			
: PRIOR FILING DATE: 2000-03-29			
: PRIOR APPLICATION NUMBER: US 60/185,218			
: PRIOR FILING DATE: 2000-02-24			
: PRIOR APPLICATION NUMBER: US 60/167,363			
: PRIOR FILING DATE: 1999-11-23			
: PRIOR APPLICATION NUMBER: US 60/156,358			
: PRIOR FILING DATE: 1999-09-28			
: PRIOR APPLICATION NUMBER: US 60/146,002			
: PRIOR FILING DATE: 1999-08-09			
: NUMBER OF SEQ ID NOS: 325720			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 113788			
: LENGTH: 3252			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:55:11 ; Search time 3703.9 seconds
(without alignments)
5952.094 Million cell updates/sec

Title: US-09-072-994A-13

Perfect score: 1019
Sequence: 1 ATGACAGTTCAGATTATTA.....TTACATTAATTGTTGATTG 1019

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pna/US083.COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US084.COMB.seq:*
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12: /cgn2_6/ptodata/1/pna/US088.COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089.COMB.seq:*
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24: /cgn2_6/ptodata/1/pna/US096B.COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US096C.COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096D.COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E.COMB.seq:*
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30: /cgn2_6/ptodata/1/pna/US097C.COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US098A.COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US098B.COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098C.COMB.seq:*
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36: /cgn2_6/ptodata/1/pna/US099C.COMB.seq:*
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39: /cgn2_6/ptodata/1/pna/US6000.COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US6001.COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US6002.COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US6003.COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US6004.COMB.seq:*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1019	100.0	1019	14	US-09-072-994-13	Sequence 13, Appl
2	1019	100.0	1019	14	US-09-072-994A-13	Sequence 13, Appl
3	1019	100.0	1019	17	US-09-305-929-13	Sequence 13, Appl
4	1019	100.0	1019	17	US-09-305-929A-13	Sequence 13, Appl
5	1004.6	98.6	1020	1	PC1-US02-03687-14283	Sequence 14283, A
6	1004.6	98.6	1020	18	US-09-463-962-1	Sequence 1, Appl1
7	1004.6	98.6	1020	37	US-10-032-585-6173	Sequence 6173, App
8	1004.6	98.6	1020	37	US-10-072-851-14283	Sequence 14283, A
9	1004.6	98.6	1020	64	US-60-259-128-4099	Sequence 4099, App
10	1004.6	98.6	1020	70	US-60-314-050-6173	Sequence 6173, App
11	1003	98.4	1038	16	US-09-248-796-4351	Sequence 4351, App
12	1003	98.4	1038	48	US-60-096-409-4351	Sequence 4351, App
13	262	25.7	262	51	US-60-127-461-3643	Sequence 6643, App
14	260.4	25.6	262	51	US-60-127-461-3655	Sequence 3655, App
15	258	25.3	260	51	US-60-127-461-6591	Sequence 6591, App
16	252.4	24.8	277	51	US-60-127-461-6911	Sequence 6291, App
17	221.8	21.8	250	51	US-60-127-461-4921	Sequence 4911, App
18	85.8	8.4	223320	63	US-60-242-679-528	Sequence 528, App
19	85	8.3	1770	28	US-09-703-708-6286	Sequence 6286, App
20	85	8.3	1770	55	US-60-164-320-6286	Sequence 6286, App
21	85	8.3	1770	57	US-60-183-791-6286	Sequence 6286, App
22	83.6	8.2	1326	26	US-09-663-779-8205	Sequence 8205, App
23	82.8	8.1	899	22	US-09-565-306-24647	Sequence 24647, A
24	82.8	8.1	1016	59	US-60-207-458-33653	Sequence 33653, A
25	82.6	8.1	1143	59	US-60-207-458-36757	Sequence 36757, A
26	82	8.0	1770	28	US-09-703-708-6286	Sequence 6286, App
27	82	8.0	1770	55	US-60-164-320-6286	Sequence 6286, App
28	82	8.0	1770	57	US-60-183-791-6286	Sequence 6286, App
29	81.8	8.0	13859	35	US-09-950-083-10355	Sequence 10355, A
30	80.6	7.9	1326	26	US-09-663-779-8205	Sequence 8205, App
31	79	7.8	223320	63	US-60-242-679-528	Sequence 528, App

SUMMARIES

32	77	7.6	192013	63	US-60-248-823-33	Sequence 33, Appl
33	76.2	7.5	98573	63	US-60-248-505-542	Sequence 542, Appl
C 34	75.6	7.4	1033	28	US-09-705-926-1603	Sequence 1603, A
35	75.4	7.4	1680	16	US-09-248-796-4378	Sequence 4378, A
36	75.4	7.4	1680	48	US-09-096-409-4378	Sequence 4378, Ap
C 37	75	7.4	11062	56	US-60-173-464-19056	Sequence 19056, A
38	74.6	7.3	11744	17	US-09-387-720-1	Sequence 1, Appl
39	74.6	7.3	11744	48	US-60-098-690-1	Sequence 1, Appl
C 40	74.6	7.3	192014	63	US-60-248-823-33	Sequence 33, Appl
41	74.4	7.3	32768	62	US-60-234-446-433	Sequence 433, A
C 42	74.2	7.3	1141	31	US-09-806-708-422	Sequence 22, Appl
43	73.8	7.2	22350	63	US-60-245-228-17	Sequence 17, Appl
44	73.4	7.2	1190	59	US-60-207-458-36950	Sequence 36950, A
45	73.2	7.2	988	26	US-09-666-355A-774	Sequence 774, A

ALIGNMENTS

```

RESULT 1
US-09-072-994-13
: Sequence 13, Application US/09072994
: GENERAL INFORMATION:
: APPLICANT: Cottarel, Guillaume
: APPLICANT: Damagnez, Veronique
: APPLICANT: Draela, Guilo
: TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
: human Pathogens, and Uses Related Thereto
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley, Hoag & Eliot, LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/072.994
: FILING DATE: 05-MAY-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV032.02
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1019 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cdna
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1017
: US-09-072-994-13

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[illegible]

QY	121	GATTTCAGTCTTCACCAACATCAATCCATCGAGAAATTTTATCTATAAACTTTGAAA	180
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QY	181	CCACATCCAAACAAATATGAAATTTTAAAGATCTTAATAAATTAATGATGATATATTA	240
Db	181	CCACATCCAAACAAATATGAAATTTTAAAGATCTTAATAAATTAATGATGATATATTA	240
QY	241	GTCCACAAATTTGTATCGTTATGATTTTGAGTCATTTGATGAAATTCAAAATATTGTAAA	300
Db	241	GTCCACAAATTTGTATCGTTATGATTTTGAGTCATTTGATGAAATTCAAAATATTGTAAA	300
QY	301	CGAACACACAGATTTATTTATGATTAATGGTAATCTTGTGTGATATCAATTAACACT	360
Db	301	CGAACACACAGATTTATTTATGATTAATGGTAATCTTGTGTGATATCAATTAACACT	360
QY	361	GCTATGCAATTAAGCAAAAGAAAGATCAATCAATTTATGTTTAAATCAATGAGTTCAGACTT	420
Db	361	GCTATGCAATTTGAAGAAAAAGATCAATCAATTTATGTTTAAATCAATGAGTTCAGACTT	420
QY	421	GAATTTATTCATTACCAAGGATTAATTCATCGATATTAACCCGATATATTCTTT	480
Db	421	GAATTTATTCATTACCAAGGATTAATTCATCGATATTAACCCGATATATTCTTT	480
QY	481	GCCCGGATGATATTAACACAACCATTATTGGAGATTTTGATATTTGTTATGATTTAAA	540
Db	481	GCCCGGATGATATTAACACAACCATTATTGGAGATTTTGATATTTGTTATGATTTAAA	540
QY	541	CTGCCACCTAAAGATGAACCCCTATGGCAATATTTGATGATCTACAGATATTAT	600
Db	541	CTGCCACCTAAAGATGAACCCCTATGGCAATATTTGATGATCTACAGATATTAT	600
QY	601	AAAGACACAGATTTGATTTCTTGATTACTAATTAATGAATGAATTTGATTTGCTCA	660
Db	601	AAAGACACAGATTTGATTTCTTGATTACTAATTAATGAATGAATTTGATTTGCTCA	660
QY	661	TTGGGTATTAATTTGACGTGGTTTATATTCCAGAAATTTTCAAGTGGTTTAGCCAAAGAT	720
Db	661	TTGGGTATTAATTTGACGTGGTTTATATTCCAGAAATTTTCAAGTGGTTTAGCCAAAGAT	720
QY	721	GATTAAGAAATGACATAATGATTCATGTTAGTATGATTTATATTAAATCAAAATATT	780
Db	721	GATTAAGAAATGACATAATGATTCATGTTAGTATGATTTATATTAAATCAAAATATT	780
QY	781	GAAAAATTCGGTACACCCAAATTTAACTGATTTTGAGATGAATTAATTTTGATGAAT	840
Db	781	GAAAAATTCGGTACACCCAAATTTAACTGATTTTGAGATGAATTAATTTTGATGAAT	840
QY	841	AATATGAAACCTGCAATTTTAAAAAATTCATTTTAAAGAAATTCCTAGAAAAGATTGG	900
Db	841	AATATGAAACCTGCAATTTTAAAAAATTCATTTTAAAGAAATTCCTAGAAAAGATTGG	900
QY	901	GATATTTATTTACCTCGATGCAATGATGATTTTAATGAAGAAATTTTACCAGATGAT	960
Db	901	GATATTTATTTACCTCGATGCAATGATGATTTTAATGAAGAAATTTTACCAGATGAT	960
QY	961	AGATATGATTCGAAGTAAAGAAATTAACCTCTAAAGAAATTCACAAATTAAGTTGGATTG	1019
Db	961	AGATATGATTCGAAGTAAAGAAATTAACCTCTAAAGAAATTCACAAATTAAGTTGGATTG	1019

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: RESULT 2
: US-09-072-994A-13
: Sequence 13, Application US/0907299A
:
: GENERAL INFORMATION:
:
: APPLICANT: Cottarel, Guillaume
:
: Draetta, Veronique
:
: TITLE OF INVENTION:
: Draetta, Guilo
: Cell-Cycle Regulatory Proteins from
: Human Pathogens, and Uses Related Thereof
:
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:

```

```

ADDRESSSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,994A
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,090
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-032.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1017
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-072-994a-13

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Query Match      100.0%; Score 1019; DB 14; Length 1019;
Best Local Similarity 100.0%; Pred. No. 9,8e-159;
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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E3 1 ATGAGTGTGCAGATTTTATATAGACAAAGCATTAATTCACATGTCGCCATTTCTGAT 60
QY 61 ATATATACGGCTATTTGATTAAGTTAATTAACCTACAGATGTCCTTAATAATGATGAA 120
Db 61 ATATATACGGCTATTTGATTAAGTTAATTAACCTACAGATGTCCTTAATAATGATGAA 120
QY 121 GATTTCAGTCTCCACACATTCATCCAGCAAGAAATTTTATACCTTAACCTTGAAA 180
Db 121 GATTTCAGTCTCCACACATTCATCCAGCAAGAAATTTTATACCTTAACCTTGAAA 180
QY 181 CCAATCCAAACATTAATTTGAATATTTTAATGATCTTAATAATTTATGATGATTAATTA 240
Db 181 CCAATCCAAACATTAATTTGAATATTTTAATGATCTTAATAATTTATGATGATTAATTA 240
QY 241 GTCACCAATTTGATGCTTATGATTTGAGTCATTAATGATGAATTAACAATAATTTGATAA 300
Db 241 GTCACCAATTTGATGCTTATGATTTGAGTCATTAATGATGAATTAACAATAATTTGATAA 300
QY 301 CGAACACACAGATTTATTTGATTAATGATTAATCTTGTGTGATGATCAATATACACTT 360
Db 301 CGAACACACAGATTTATTTGATTAATGATTAATCTTGTGTGATGATCAATATACACTT 360
QY 361 GCTATATGAAATTTGAGAAAAAGATATCAATTAATGCTTAATAATCAATGATGACACTT 420
Db 361 GCTATATGAAATTTGAGAAAAAGATATCAATTAATGCTTAATAATCAATGATGACACTT 420
QY 421 GAATTTTTCATTCACAGGATTAATTCATGATATTAACCCGCTAATTTTCTT 480

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Db 421 GAATTTTTCATTCACAGGATTAATTCATGATATTAACCCGCTAATTTTCTT 480
QY 481 GCCGGGATGATTAATACACAAACGATTAATGAGATTTGATATTTGATGATTTAAA 540
Db 481 GCCGGGATGATTAATACACAAACGATTAATGAGATTTGATATTTGATGATTTAAA 540
QY 541 CTGCCACCTTAACATGACCCCTATGCGGAAATATATTGATATCTACAGATTTAT 600
Db 541 CTGCCACCTTAACATGACCCCTATGCGGAAATATATTGATATCTACAGATTTAT 600
QY 601 AAAGCACCAGAAATTCATCTGTATTAATTAATTAATGATTAATGATTAATTTGTCGA 660
Db 601 AAAGCACCAGAAATTCATCTGTATTAATTAATTAATGATTAATGATTAATTTGTCGA 660
QY 661 TTGGGATTAATTTGACGTGTTATATTCAGAAAATTTTCAAGTGTTTTACGCAAGAT 720
Db 661 TTGGGATTAATTTGACGTGTTATATTCAGAAAATTTTCAAGTGTTTTACGCAAGAT 720
QY 721 GATTAAGAAATTCATGATGATCTCATGTTAGATTTATTTATTTAATCAATATTT 780
Db 721 GATTAAGAAATTCATGATGATCTCATGTTAGATTTATTTATTTAATCAATATTT 780
QY 781 GAAAATTTCCGTACACCAATTTAAGATGATTTTGAAGATGATTTATTTGTATGAATAT 840
Db 781 GAAAATTTCCGTACACCAATTTAAGATGATTTTGAAGATGATTTATTTGTATGAATAT 840
QY 841 AATATGAAACCTGCTTTTAAATAATTCATTTCAAAATATCCATGGAAGAAATTTG 900
Db 841 AATATGAAACCTGCTTTTAAATAATTCATTTCAAAATATCCATGGAAGAAATTTG 900
QY 901 GATTTATTTTACCCTGAGCAATGATGATTTATGAAGAAATTTTACCAAGATGAT 960
Db 901 GATTTATTTTACCCTGAGCAATGATGATTTATGAAGAAATTTTACCAAGATGAT 960
QY 961 AGATATGATGAAGTAAAGATTAATCTCAAAAGAAATCTCAATTAATGTTGATTTG 1019
Db 961 AGATATGATGAAGTAAAGATTAATCTCAAAAGAAATCTCAATTAATGTTGATTTG 1019

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RESULT 3
US-09-305-929-13
; Sequence 13, Application US/09305929
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cyclin Activating Kinase (CAK) from Human
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,929
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,090
; FILING DATE: 05-JUN-1995
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1017
; US-09-305-929-13

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Query Match      100.0%; Score 1019; DB 17; Length 1019;
Best Local Similarity 100.0%; Pred. No. 9,8e-159;
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 ttgggtataatttcgacggttataatccagaattccaaagtgctttagtcaagaat 720
QY 721 GATAAAGATTCGACTAATGATTCATGTTAGTGATTTATATTTTAAATCAATATTT 780
Db 721 gataaagatttgacaaatgattctcaatgttagtgattataatcttaacaaatattc 780
QY 781 GAAAAATTCGTGACACCCAAATTTAACTGATTTTGAAAGATTAATTTTGTGATGAATAT 840
Db 781 gaaaatttcgtagcaccacaaatttaactgattttagaagtataatttcttgatgaatat 840
QY 841 AATATGAAGAACTTCGATTTTAAAAATTCATTTACAAAAATATCCAGAAAAAGATTGG 900
Db 841 aataatgaaaacctgcattcttaaaaaattcaattcaaaaaataccctagaanaagattgg 900
QY 901 GATATTTATTTTACCTCGATGCAATGATGATTTAATGAAGAAATTTTACCAAGATGAT 960
Db 901 gatattatttaccctcgatgcagtatgatttaataagaanaattttccaagaatgatt 960
QY 961 AGATATGATCGAAGTAAAGAAATTAACCTCTAAGAAATCTTACAAATTAATGTTGATG 1019
Db 961 agatatgacgaagtaaaaagaataacttctaagaanaattccaatgaattgtagattg 1019
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RESULT 5

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PCT-US02-03987-14283
; Sequence 14283, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA 028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14283
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
PCT-US02-03987-14283
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-Query Match 98.68; Score 1004.6; DB 1; Length 1020;

Best Local Similarity 99.18; Pred. No. 2.3e-156;

Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATGAAGTTGTAGATTTATATATAGACAGGAATTAATTAACATNCTGCCATTTCGAT 60
Db 1 atgaagttgtcagattatataagacaagaaatttaacttaagtcgcatctcgat 60
QY 61 ATATATACGGCTATTGATTAAGTTTAACTTACAGTATGCTTAAATAGTTGATGAA 120
Db 61 atataacggtattgataagtttaacttaacttaaccagtaagtccttaaaatagttgatgaa 120
QY 121 GATTTCAGCTCTCCACACACATTCATTCATCGAGAAATTTTATCTTAAACTTTGAAA 180
Db 121 gatttcagctctccacacacatctcaatccaggaagttcttataacttaaaactttgaaa 180
QY 181 CCACATCCAAACATTAATGAATATTTTAATGATCTTAAATTAATGATGTTATATTA 240
Db 181 ccacatccaaacataatgataattttaagacccctaaatctgtagcagatataata 240
QY 241 GTCAACCAATTTGATGCTTATGATTTGAGTCAATTGATTAATTAACAAATTTGTAA 300
Db 241 gtccaacaaattgactgattagtgagtcgaattgtagaattcaaaaattgtgaa 300
QY 301 CGAACACACAGATTTATTTATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
Db 301 cgaaacacagatttattatgtagtataatgtaattcttgtagtaataataatacatt 360
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QY 361 GCTAATGAATAATGAGAAAAAGATATCAATTAATGTTAAATCAATGATTCAGGACT 420
Db 361 gctaataaattgaagaaaaagataataaatttggttaataacaaatggtccaagact 420
QY 421 GAATTTATTCATTCACAAAGGATTAATTCATCGATATATAAAACCCAGTAATATTTCTTT 480
Db 421 gaatttattcatccaaggaataattcatcgcgataataaaccataatttcttctt 480
QY 481 GCCCGGATATATTAACACAAACCGATTATGAGATTGATATTTGTTATGATTTAAA 540
Db 481 gcccggaatgataacaacaacgaattatgagatttgatataagttatgattatgataaa 540
QY 541 CTGCGACCTAAAGATGAAACCCCTATGCGGAATTAATGATGATCTACAGTATTTAT 600
Db 541 ctgcgacctaaagatgaacccctatgcggaataatataatgatactctcaagttatc 600
QY 601 AAAGCACGCAATTTGATTTCTTGCTATTAATTAATGAAATTAATGATTTGGTCA 660
Db 601 aaagcaccaagattgattcttgatataactaattatgataatgaattgatatltgca 660
QY 661 TTGGGTATATTTTGACTGCTGTTATATTCAGAAATTTCAAGTGTTTTACTCAAGAT 720
Db 661 ttgggtataatttcgactggtttatatacagaattttccaagtgtttagtcaagaat 720
QY 721 GATAAAGAAATTCATGATTCATGTTAGTATTAATTAATTAATCAATATTT 780
Db 721 gataaagaatttgactaattctcatctcagtttagtgattataatttaataataattt 780
QY 781 GAAAAATTCGTGACACCCAAATTAACGATTTTGAAGATGAATTAATTTGTGATGAAT 840
Db 781 gaaaatttcgtagcaccacaaatttaactgatttgaagaagaaatttcttgatgaatat 840
QY 841 AATATGAAGAACTTCGATTTTAAAAATTCATTTCAAAAAATATCCTGAAGAAAGTTGG 900
Db 841 aataatgaaaacctgcattcttaaaaaattcaattcaaaaaataccctagaanaagattgg 900
QY 901 GATATTTATTTTACCTCGATGCAATGATGATTTAATGAAGAAATTTTACCAAGATGAT 960
Db 901 gatattatttaccctcgatgcagtatgatttaataagaanaattttccaagaattgatt 960
QY 961 AGATATGATCGAAGTAAAGAAATTAACCTCTAAGAAATCTTACAAATTAATGTTGATG 1019
Db 961 agatatgacgaagtaaaaagaataacttctaagaanaattccaatgaattgtagattg 1019
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RESULT 6

US-09-463-962-1

; Sequence 1, Application US/09463962

; GENERAL INFORMATION:

; APPLICANT: FAYE, GERARD

; APPLICANT: VALAY, JEAN-GABRIEL

; APPLICANT: MANN, CARL

; APPLICANT: THURET, JEAN-YVES

; TITLE OF INVENTION: KINASE ACTIVATING DEPENDENT CYCLIN PROTEIN KINASES AND THEIR

; FILE REFERENCE: 0846-0536-0XPCT

; CURRENT APPLICATION NUMBER: US/09/463,962

; PRIOR APPLICATION NUMBER: PCT/FR98/01788

; PRIOR FILING DATE: 1998-08-11

; PRIOR APPLICATION NUMBER: FR97/10287

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patent version 3.0

; SEQ ID NO 1

; LENGTH: 1020

; TYPE: DNA

; ORGANISM: Candida albicans

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1020)

; US-09-463-962-1

Query Match 98.6%; Score 1004.6; DB 18; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATGAAGTTGTCAGATTATTTATATAGACAAAGAAATTAATTTACAAATAGTGCATTTCTGAT 60
    |||||
Db 1 atgaagttgctcagattatattatataagacaagaaatttaattacaatagcgatcttcgat 60
QY 61 ATATATACGGCTATTTGATTAAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 120
    |||||
Db 61 atataatgctcagattatattatataagttacaatgctcagattatattatataagttatgaa 120
QY 121 GATTTCAGTCTTCACACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 180
    |||||
Db 121 gatttcagcttcacacatcattcaatccatcgagaagttcttatacttaaaacttggaa 180
QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
    |||||
Db 181 ccacatccaaacataattgaatttaattgaatttaattgaatttaattgaatttaattga 240
QY 241 GTACACCAATTTGATTCGTTATGATTTGATTCGTTATGATTTGATTCGTTATGATTTGATTT 300
    |||||
Db 241 gtacaccaatctgatacgtatgatttgaatttgaatttgaatttgaatttgaatttgaatt 300
QY 301 CGAACACACAGATTATTTATGTTATTAATGTTATTAATGTTATTAATGTTATTAATGTTAT 360
    |||||
Db 301 cgaacacacagattattattatgatttgaatttgaatttgaatttgaatttgaatttgaatt 360
QY 361 GCTAATGAATTTGAGAAAAAGATATCAATTAATGTTTAAATGCAATGAGTTGACAGACTT 420
    |||||
Db 361 gctaatgaatttgaagaaaaagataccaattatggtttaaacaatgagttcagagactt 420
QY 421 GAATTAATTCATTCACACAGGATTAATTCGTTATTAATTAATTAATTAATTAATTAATTA 480
    |||||
Db 421 gaattatcatcacaagagataatcatcgtatataataaaccagtaatttctt 480
QY 481 GCCCGGATGATTAACACACCGATTATTTGAGATTTTGAATTTGATTTGATTTGATTTGAT 540
    |||||
Db 481 gcccggatgataatacacaacgattatttgaatttgaatttgaatttgaatttgaatttga 540
QY 541 CTGCCACCTTAAGATGAACCCCTATGCGGAATATTAATGATTAATTAATTAATTAATTA 600
    |||||
Db 541 ctgccaccttaagatgaacccctatgcggaatattatgatttgaatttgaatttgaatttga 600
QY 601 AAAGCACAGAAATTTGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
    |||||
Db 601 aaagcacagaaatttgaatttgaatttgaatttgaatttgaatttgaatttgaatttga 660
QY 661 TTGGGTATTAATTTGACGTGTTATATTCAGAAAAATTTTCAAAAGTCTTACTCAAAAGAT 720
    |||||
Db 661 ttgggtatataatttgaactggttataatccaagaatttcaaaagtcttactcaaaagat 720
QY 721 GATAAAGAAATTTGACTAATGTTCTCATGTTAGTATTAATTAATTAATTAATTAATTAAT 780
    |||||
Db 721 gataaagaatttgaactaattctcatggttgaatttgaatttgaatttgaatttgaatttga 780
QY 781 GAAAATTTGCGTACACCAATTTTACTGATTTTGAAGATTAATTAATTTGTTGATGAATAT 840
    |||||
Db 781 gaaaatttgcgtacaccacaatttactgatttgaagatgaatttgaatttgaatttgaatt 840
QY 841 AATAAAGAAAATCTTGCAATTTTAAAAATTCATTTTCAAAAAATATCTTGAAAAAGATTGG 900
    |||||
Db 841 aataaagaaaacttgcattttaaaaaattcaatttcaaaaaatctcctaagaaaagtgg 900
QY 901 GATATTATTTTACTCGATGCAATGATGATTTAATGAAGAATTTTTCGCAAGATGATTT 960
    |||||
Db 901 gatattatatttactcgtatgcaatgatatattcaatgaagaatttcttccaaagtatt 960
QY 961 AGATATGATCGAAGTAAAAAGAAATTAATTTCAAAAGAAATCTTCAAAATTAATTTGTTGA 1019
    |||||
Db 961 agatgatcgaaagtaaaagaataactctcaagaatacttcaaatatagttgaattg 1019
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RESULT 7

US-10-032-585-6173
; Sequence 6173, Application US/10032585
; GENERAL INFORMATION:

; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jjiang
; APPLICANT: Charles, Boone

; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

; FILE REFERENCE: 10102-005-999
; CURRENT APPLICATION NUMBER: US/10/032, 585

; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6173

; LENGTH: 1020
; TYPE: DNA

; ORGANISM: Candida albicans
; US-10-032-585-6173

Query Match 98.6%; Score 1004.6; DB 37; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATGAAGTTGTCAGATTATTTATATAGACAAAGAAATTAATTTACAAATAGTGCATTTCTGAT 60
    |||||
Db 1 atgaagttgctcagattatattatataagacaagaaatttaattacaatagcgatcttcgat 60
QY 61 ATATATACGGCTATTTGATTAAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 120
    |||||
Db 61 atataatgctcagattatattatataagttacaatgctcagattatattatataagttatgaa 120
QY 121 GATTTCAGTCTTCACACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 180
    |||||
Db 121 gatttcagcttcacacatcattcaatccatcgagaagttcttatacttaaaacttggaa 180
QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
    |||||
Db 181 ccacatccaaacataattgaatttaattgaatttgaatttgaatttgaatttgaatttga 240
QY 241 GTACACCAATTTGATTCGTTATGATTTGATTCGTTATGATTTGATTCGTTATGATTTGATTT 300
    |||||
Db 241 gtacaccaatctgatacgtatgatttgaatttgaatttgaatttgaatttgaatttgaatt 300
QY 301 CGAACACACAGATTATTTATGTTATTAATGTTATTAATGTTATTAATGTTATTAATGTTAT 360
    |||||
Db 301 cgaacacacagattattattatgatttgaatttgaatttgaatttgaatttgaatttgaatt 360
QY 361 GCTAATGAATTTGAGAAAAAGATATCAATTAATGTTTAAATGCAATGAGTTGACAGACTT 420
    |||||
Db 361 gctaatgaatttgaagaaaaagataccaattatggtttaaacaatgagttcagagactt 420
QY 421 GAATTAATTCATTCACACAGGATTAATTCGTTATTAATTAATTAATTAATTAATTAATTA 480
    |||||
Db 421 gaattatcatcacaagagataatcatcgtatataataaaccagtaatttctt 480
QY 481 GCCCGGATGATTAACACACCGATTATTTGAGATTTTGAATTTGATTTGATTTGATTTGAT 540
    |||||
Db 481 gcccggatgataatacacaacgattatttgaatttgaatttgaatttgaatttgaatttga 540
QY 541 CTGCCACCTTAAGATGAACCCCTATGCGGAATATTAATGATTAATTAATTAATTAATTA 600
    |||||
Db 541 ctgccaccttaagatgaacccctatgcggaatattatgatttgaatttgaatttgaatttga 600
QY 601 AAAGCACAGAAATTTGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
    |||||
Db 601 aaagcacagaaatttgaatttgaatttgaatttgaatttgaatttgaatttgaatttgaatt 660
QY 661 TTGGGTATTAATTTGACGTGTTATATTCAGAAAAATTTTCAAAAGTCTTACTCAAAAGAT 720
    |||||
Db 661 ttgggtatataatttgaactggttataatccaagaatacttcaaatatagttgaattg 720
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QY 721 GATTAAGATGACTAATGATTCTCATGTTAGTATTATATTATTAATCAAAATATT 780
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Db 721 gataaagaattgactaatgatctcatgtagtattatattataatcaaatatt 780
QY 781 GAAATTTGGGTACGCCAATTTAACTGATTTTGAAGATGATTTTGTGATGANTT 840
      |||
Db 781 gaaaatctgtagcaccacatttaactgatttgaagaagaatttcttgatgaatt 840
QY 841 AATAATGAAACTTGCATTTTAAAAATTCATTTTACAAAAATATCCTGAAAGATTGG 900
      |||
Db 841 aataaagaactgtagtatttaaaaaattcaatttcaaaaaataccctagaagaattgg 900
QY 901 GATATTATTTTACCTGATGCAATGATGATTTAATGAAGAATTTTACCAAGATGAT 960
      |||
Db 901 gatattatttaccctcgatgcaatgtagtatttcatgaaagaatttttccaagatgat 960
QY 961 AGATATGATCGAAGTAAAGAATTAAGTCTTAAAGAAATCTTCAATTAATGTTGATTTG 1019
      |||
Db 961 agatatgtagcgaagtaagaataaactcttaagaagaaccttaaatgtagattg 1019

RESULT 8
US-10-072-851-14283
; Sequence 14283, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072.851
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14283
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-072-851-14283

Query Match 98.6%; Score 1004.6; DB 37; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGAAGTTGTCGATTATTATATAGACAAGAATTAATTTACAAATAGCCATTTCAT 60
      |||
Db 1 atgaagttgtagcatattatatatagacaagaattaattcaaatagcgcatcttgat 60
QY 61 ATATTTAGGCGTATTTGATAAGTTTAATTAACCTTACCAGTATCTTTAAATAGTTGATCAA 120
      |||
Db 61 atatacggcatatgataaagtttaataacttaccagatgcttctaataatagttgagaa 120
QY 121 GATTTCAGTCTTCACACCATTTCAATTCATGAGAAATTTTATATCTTAAGTTAAACTTTGAAA 180
      |||
Db 121 gatttcagcttctccacacatccaatccaatcgagaagttcttcaacttaaaacttgaaa 180
QY 181 CCACATCCAAACATTAATTAATTTAATGATCTTAAATTTAATGATGATGATATATTA 240
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Db 181 ccacatccaaacataaattgaatattttaaagtatctttaaatttctgacgatattatcta 240
QY 241 CTCACCAAAATTTGATCGTTATGATTTGAGCAATTTGATGAAATTTACAAAATATTGTAAA 300
      |||
Db 241 gtcaccaaattgtagcttgaattgatttggcgaatttgattgaattacaataatttga 300
QY 301 CGAACAAACAGATTATTTATGTTAATGTTAATCTGTTACTAATCAATATACACTT 360
      |||
Db 301 cgaacaacacgatttaattatcagcatlaaaggtaaccttgtagtaacatacacactt 360
QY 361 GCTAATGAAATTTGAAGAAAAGATATCAATTAATGTTTAAATCAATGAGTTCGACTT 420
      |||
Db 361 gctaataaatttgaagaaaagatatcaaatatagtttaaatcaatgaattcagaactt 420
QY 421 GAATTTATTTCACTACCAAGGATTAATTCATCTGATATTTAAACCAGTAATATTTCCTT 480
      |||
Db 421 gaattattcatcacaaggagtaattcatatgtagataaaaccataatatttctt 480
QY 481 GCCCGGATGATATTAACACAAACCGATTATTGAGATTGTTGATTTGATTTTAAA 540
      |||
Db 481 gcccgagtagatataacacaaccgattatggagattttagattagttatgatttaaaa 540
QY 541 CTGCCACCTAAAGATGAACCCCTATGCGGAATATATGATGATCTACAGGTAATTTAT 600
      |||
Db 541 ctgcacacctaaagatgaacccccctatgscgaatatatatgtagtactacaagttatt 600
QY 601 AAGACACAGAAATTTGATTTGTTGTTAATTAATTAATGAATGAATTTGATTTTGTCA 660
      |||
Db 601 aaagacacagaattgattcttggatataaccaatlaagaaatgaaattgatttggta 660
QY 661 TTGGGTATTAATTTTACTGTTTATATTCAGAAAATTTTCAAGTGTTTAGTCAAAAGAT 720
      |||
Db 661 ttgggtataattttagctgttttatcttcagaaatttcaaaagtgtttagtcaaaagt 720
QY 721 GATAAAGAATTTGATTAATGATTTCTCAGTTAGTGATTTTATTTAATTAATTAATTTT 780
      |||
Db 721 gataaagaattgactaagttctcagtttagttagtattatatttaaatcaaatatt 780
QY 781 GAAATTTGCGTACACCAATTTAACTGATTTTGAAGATGAATTTTGTGATGAATAT 840
      |||
Db 781 gaaatttgcgtacacccaatttaaccgatttgaagatgaattatcttgtagatatt 840
QY 841 AATATGAAAACTTGATTTTAAAAATTCATTTTCAAAAATATCTAGAAAAAGATTGG 900
      |||
Db 841 aataatgaaaacttgcatctttaaanaattcaatttcaaaaataatcctgaaagaatttg 900
QY 901 GATTTTATTTTACCTGATGCAATGATGATTTTAATGAAAAAATTTTACCAAGATGAT 960
      |||
Db 901 gattatttaccctcgatgcaatgtagtatttcaatgaagaatttttccaagatgat 960
QY 961 AGATATGATCGAAGTAAAGAATTAAGTCTTAAAGAAATCTTACAAATTAATGTTGATTTG 1019
      |||
Db 961 agatatgtagcgaagtaagaataaactcttaagaagaaccttaaatatgtagattg 1019

RESULT 9
US-60-259-128-4099
; Sequence 4099, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4099
; LENGTH: 1020
; TYPE: DNA
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ORGANISM: Candida albicans
US-60-259-128-4099

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Query Match          98.6%; Score 1004.6; DB 64; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAGAGTTGTCAGATTATATATAGACAGAGAAATTAATTTACAATAGAGCCATTTCGAT 60
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Db 1 atgaagttgctcagattatataatagacaagaaatlaattacaatagtcgacatttcgat 60

QY 61 ATATATACGGCTATTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
   |||||||
Db 61 atataacggctattgataagtttaacttaaccagatagtccttaaaatagttgagaa 120

QY 121 GATTTCAGTCTTCACACCATTCATCCATCGAGAGAAATTTTATACCTTAAACTTTGAAA 180
   |||||||
Db 121 gatttcagtccttcacacatccaatccaatcgagaagttcttatacttaaaacttggaaa 180

QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
   |||||||
Db 181 ccacatccaaacaataatgaatatttcaatcttcaaaacttggagaatattatata 240

QY 241 GTCCACCAATTTGATGCTTATGATTTGATTCATTTGATTTGATTTGATTTGATTTGATTT 300
   |||||||
Db 241 gtccaccaatttgatcgttatgattgagtcgaattgattgaaattacaatatctgtaa 300

QY 301 CGAACACACAGATTTTATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
   |||||||
Db 301 cgaaacacacagatttattatgattatgaatcgttgaatcaataatacaactt 360

QY 361 GCTAATGAATTTGAGAAAAAGATATCAATTAATGATTAATGATTAATGATTAATGATTA 420
   |||||||
Db 361 gctaaatgaattgaagaaaaagatatacaattatgattaaatcgaagttccagact 420

QY 421 GAATTTATTCATTCACAGGGATTAATTCATCGATTAATTAATTAATTAATTAATTAATTT 480
   |||||||
Db 421 gaatttatcatccaaggaataatcatcgtgataaaacccaattatatttcttct 480

QY 481 GCCCGGATGATTAACACACACGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTT 540
   |||||||
Db 481 gccccggatgattaaacacacgattatgagattgagatctgtaactgtaattaaa 540

QY 541 CTCGCAACCTTAAGATGAACCCCTATGGCAAAATTAATTAATTAATTAATTAATTAATTT 600
   |||||||
Db 541 ctgcacaaccttaagatgaacccctatggcaaaattatgattatctacaggtattat 600

QY 601 AAAGCACCAGATTTGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTTG 660
   |||||||
Db 601 aaagcaccagattgattcttctgtaataacttaataatgaatattgatatltggtca 660

QY 661 TTGGGTATTAATTTGACTGTTATTAATTTGAGAAAAATTTTCAAGGTCTTTAGTCAAGAT 720
   |||||||
Db 661 ttgggtataatttgactggttataatctcagaataattccaagtgctttagtcaagat 720

QY 721 GATTAAGCAATTTGACTAATGATTTCTCATGTTAGTGAATTAATTAATTAATTAATTT 780
   |||||||
Db 721 gattaagcaatttgactaattgattctcatgttagtgattatatttaataatcaatatt 780

QY 781 GAAAATTTGCGTACACCAATTTAATGATTTGAGAGATTAATTTTGTGTGAATTAAT 840
   |||||||
Db 781 gaaaatttgctgtaacccaatttaactgatttgaagaatgaattattcttggatgaat 840

QY 841 AATAATGAAGCTTGAATTTTAAATAATTAATTTTCAAAAAATATCTTGAGAAAGATTTGG 900
   |||||||
Db 841 aataatgaagcttgcaattttaaataatcaatttaaaaaatatacttgagaaagattgg 900

QY 901 GATATTTATTTACCTCGATCAATGATGATTAATGAAGAAAAATTTTACCAAGATGATTT 960
   |||||||
Db 901 gatattttactcctcgatcgatgattgattcatgtaagaataattttccaagatgatt 960

QY 961 AGATATGATCGAAGTAAAGAAATTAATCTTAAGAAATCTTACAATTAATGTTGGATTTG 1019
   |||||||
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Db 961 agatattgctgaagtaagaataacttcaagaagaatcttaacatgaattgtaagttg 1019

RESULT 10
US-60-314-050-6173
; Sequence 6173, Application US/60314050
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Boosey, Charles
; APPLICANT: Bussey, Howard
; APPLICANT: Ohlson, Karl L.
; TITLE OF INVENTION: GENE DISRUPTION METHODOLOGIES FOR DRUG TARGET DISCOVERY
; FILE REFERENCE: 10182-013-888
; CURRENT APPLICATION NUMBER: US/60/314, 050
; NUMBER OF SEQ ID NOS: 7834
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6173
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
US-60-314-050-6173

Query Match          98.6%; Score 1004.6; DB 70; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAGAGTTGTCAGATTATATATAGACAGAGAAATTAATTTACAATAGTGCATTTTCGAT 60
   |||||||
Db 1 atgaagttgctcagattatataatagacaagaaatlaattacaatagtcgacatttcgat 60

QY 61 ATATATACGGCTATTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
   |||||||
Db 61 atataacggctattgataagtttaacttaaccagatagtccttaaaatagttgagaa 120

QY 121 GATTTCAGTCTTCACACCATTCATCCATCGAGAGAAATTTTATACCTTAAACTTTGAAA 180
   |||||||
Db 121 gatttcagtccttcacacatccaatccaatcgagaagttcttatacttaaaacttggaaa 180

QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
   |||||||
Db 181 ccacatccaaacaataatgaatatttcaatcttcaaaacttggagaatattatata 240

QY 241 GTCCACCAATTTGATGCTTATGATTTGATTCATTTGATTTGATTTGATTTGATTTGATTT 300
   |||||||
Db 241 gtccaccaatttgatcgttatgattgagtcgaattgattgaaattacaatatctgtaa 300

QY 301 CGAACACACAGATTTTATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
   |||||||
Db 301 cgaaacacacagatttattatgattatgaatcgttgaatcaataatacaacttggaaa 360

QY 361 GCTAATGAATTTGAGAAAAAGATATCAATTAATGATTAATGATTAATGATTAATGATTA 420
   |||||||
Db 361 gctaaatgaattgaagaaaaagatatacaattatgattaaatcgaagttccagact 420

QY 421 GAATTTATTCATTCACAGGGATTAATTCATCGATTAATTAATTAATTAATTAATTAATTT 480
   |||||||
Db 421 gaatttatcatccaaggaataatcatcgtgataaaacccaattatatttcttct 480

QY 481 GCCCGGATGATTAACACACGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 540
   |||||||
Db 481 gccccggatgattaaacacacgattatgagatttgaatcttgaattgattgaattaaa 540

QY 541 CTCGCAACCTTAAGATGAACCCCTATGGCAAAATTAATTAATTAATTAATTAATTAATTT 600
   |||||||
Db 541 ctgcacaaccttaagatgaacccctatggcaaaattatgattatctacaggtattat 600

QY 601 AAAGCACCAGATTTGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTTG 660
   |||||||
Db 601 aaagcaccagattgattcttctgtaataacttaataatgaatattgatatltggtca 660
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OY 661 TTGGTATATTTTGACTGGTTATATTCAGAAAATTTTCAAAGTGTATTAGCAAAAT 720
|||||
Db 661 ttgggataatttggactggttataatctcagaagaatttccaagtglttagtccaagat 720
OY 721 GATTAAGATTTGCTATATGATTTCTCATGTTAGTATTTATTTATTAATCAATATTT 780
|||||
Db 721 gataaaagtctacataatgattctcatgttagtgatttataattataaacaatatct 780
OY 781 GAAATTTGCTACCCCAATTTAACTGATTTTGAAGATGATTTTGTGATGATAT 840
|||||
Db 781 gaaaatttggcaccaccaatttaactgatttgaagaatctcttgtagaataat 840
OY 841 AATTAATGAAACTTGCTATTTAAAAAATTCATTTACAAAATATCTAGAAAAGATTGG 900
|||||
Db 841 aataatgaaaacttgcatctttaaaaaattcaattcaaaaaatactcagaagaattgg 900
OY 901 GATATATTTTACCTCGATGCAATGATGATTTATGAAAAGAAATTTTACCAAGATGAT 960
|||||
Db 901 gataataatttaccctcgatgcaagttagattctcagaaagaatttctaccaagattg 960
OY 961 AGATATGATGCAAGTAAAGATTAATCTTAAGAAATCTTAATCAATTAATGTTGATGG 1019
|||||
Db 961 agatatgctcgaagtaaaagaataactcttaagaatactcttaactaatgttagattg 1019
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RESULT 11
US-09-248-796-4351
; Sequence 4351, Application US/09248796
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796
; NUMBER OF SEQ ID NOS: 28206
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796-4351
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Query Match 98.4%; Score 1003; DB 16; Length 1038;
Best Local Similarity 99.0%; Pred. No. 4.3e-156;
Matches 1009; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 1 ATGAAGTTGTCAGATTATTTATATAGACAAGAAATTAATTTCAATATAGCAATTTCTGAT 60
|||||
Db 19 atgaagttgctcagattatataatagacaagaatttaatttcaacaatgagccattctgatt 78
OY 61 ATATATACGGCTATTGATTAAGTTTAATTAACCTTACCAAGTATGCTTAAATAGTTGATGAA 120
|||||
Db 79 atataacggtctattgataagtttaataacttaaccagatgcttcttaaaatagttgataa 138
OY 121 GATTTACAGCTTCCACCATTCATTCATCGAGAAATTTTATTAATCTTAAACCTTTGAAA 180
|||||
Db 139 gatttcagcttccaccacattcattccatcgcagagagttcttataacttaaaacttggaaa 198
OY 181 CCACATCCAAACATTAATGAATATTTTAAATGATCTTAAATTTATGATCTATATATTA 240
|||||
Db 199 ccaactccaacaataatgataatttataatgattcttaaaatttggcagatataatata 258
OY 241 CTCACCAATTTGTATGTTATGATTTTGAAGCAATTTGATTTGAATTTACAAAATATTGTAAA 300
|||||
Db 259 gtccccaattgtatcgtatgatttggtcgaattgataatcttaacaaaatattgtaaa 318
OY 301 CGAACCAACAGATTATTTATGATTAATGTTAATGTTAATCTTGTATTAATCAATATACACTT 360
|||||
Db 319 cgaacaaacagatttataatcgtatcgtatcgtatcgtatcgtatcgtatcgtatcgtatc 378
OY 361 GCTAATGAATTTGAAGAAAAGATATCAAAATTAATGTTAAATCAATGAGTTTCAGACTT 420
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Db 379 gctaatgaaattgaaagaaagataataatctatggttaaaatcaaatgagcttcaaggact 438
|||||
OY 421 GAATTTATTCATTCACAAGGGAATTAATTCATGATTAATAAACCCAGTAATATTCTGTT 480
|||||
Db 439 gaatttattcttcaacaaggataatctcattcattgataataaaccagtaattatcttct 498
OY 481 GCCCGGATGATTAATTAACCAACCATTAATTTGGAATTTTGATTTGTTATGATTTAAA 540
|||||
Db 499 gcccggaattgataaacaacacgattatggaatttggatatttggatttggattttaa 558
OY 541 CTGCCACCTTAAGATGAACCCCTATGCGCAAAATATTTGATGATATACAGGATTTAT 600
|||||
Db 559 ctgcacactaaagttagaaccocccatagcggaataatctgattatctcaaggtattat 618
OY 601 AAAGCACCAGATTTGATTTCTTGGTATTAATTAATTAATTAATTAATTAATTAATTA 660
|||||
Db 619 aaagcaccagaattgattcttggtataactaattatgataatgaaattgatttggta 678
OY 661 TTGGGTATATTTGACGTGGTTTATTCAGAAAATTTTCAAAGTGTATTAGCAAAAGAT 720
|||||
Db 679 ttgggtataatttggactggttataatctcagaagaatttcaagtglttagtccaagat 738
OY 721 GATTAAGATTTGACTTAATGATTTCTCATGTTAGTATTTATTTATTAATCAAAATATT 780
|||||
Db 739 gataagaattgactaatgattctcattcattgattattatattataatcaaatatt 798
OY 781 GAAATTTGCGTACACCAATTTACTGATTTTGAAGATGATTAATTTGTGATGAATAT 840
|||||
Db 799 gaaaatttgcgtacacccaatttaactgatttgaagaatgaaattatttggatgaatat 858
OY 841 AATTAAGAAACTTGCAATTTTAAAAAATTCATTTCAAAAATATCTGAAAAAGATTGG 900
|||||
Db 859 aataatgaaaacttgcaattttaaataatcttaacttaacaaatactcagaagaattgg 918
OY 901 GATTTATTTTACCTCGATGCAATGATGATTTTAATGAAGAAATTTTACCAAGATGAT 960
|||||
Db 919 gataatttctacctcgatgcaagttagattctcagaagaatatttctaccaagattg 978
OY 961 AGATATGATGCAAGTAAAGATTAATCTTAAGAAATCTTAATTAATTAATGTTGATGG 1019
|||||
Db 979 agatatgctcgaagtttaaaagaataactcttaagaataactcttaactaatgttagattg 1037
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RESULT 12
US-60-096-409-4351
; Sequence 4351, Application US/60096409A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
; FILE REFERENCE: GTC-016P
; CURRENT APPLICATION NUMBER: US/60/096.409A
; NUMBER OF SEQ ID NOS: 28206
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Candida albicans
US-60-096-409-4351
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Query Match 98.4%; Score 1003; DB 48; Length 1038;
Best Local Similarity 99.0%; Pred. No. 4.3e-156;
Matches 1009; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 1 ATGAAGTTGTCAGATTATTTATATAGACAAGAAATTAATTTACAAATAGTCCATTTCTGAT 60
|||||
Db 19 atgaagttgctcagattatataatagacaagaatttaatttaacaaatgctcattctgatt 78
OY 61 ATATATACGGCTATTGATTAAGTTTAATTAACCTTACCAAGTATGCTTAAATAGTTGATGAA 120
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Db 79 atataacggtctattgataagtttaataacttaaccagatgcttcttaaaatagttgataa 138
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QY 121 GATTTCAGTCTTCACACATTCATCATCGAGAAATTTTACTTAAACTTTGAAA 180
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Db 139 gatttcagcttccacacacatccaatccatcgagaagctctctacttaaacattgaaa 198
QY 181 CCACATCCAAACATTAATGATATTTTAAATGATCTTAAATTTTATGATGATGATATTA 240
    |||||||
Db 199 ccacatccaacaataattgataatttaactgatacttaaaatttgtaacgataattatta 258
QY 241 GTGACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
    |||||||
Db 259 gtacccaactgcatcgttaagctgagcgaactgctgaactgaacaaactatgtaaa 318
QY 301 CGAACACACAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
    |||||||
Db 319 cgaaacacagctattattatgcttaagctgtaactgctgtaactgtaactaatacact 378
QY 361 GCTAATGATTAATGAGAAAAGATATCAATTTTGTTAAATCAATGATGATGATGATGAT 420
    |||||||
Db 379 gctaatgaaattgaagaaaaagatacaaatatgcttaaaatcaatgagcttcagact 438
QY 421 GAATTTTATTCATCACAGGATTAATTCATCGATGATATTAACCCAGTAAATTTTCTTT 480
    |||||||
Db 439 gaatttatcatccaagaagataatccatcgatataaaacccgataattttctt 498
QY 481 GCCCGGAGATATTAACACACACGATTTATGAGATTTTGAATTTTGAATTTTGAATTTTGA 540
    |||||||
Db 499 gcccgagatgataaacaacagatattgagactttgataattgctatgatttcaaa 558
QY 541 CTCGCCACTTAAGATGACCCCTATGCGGATATTAATGATGATGATGATGATGATGATGAT 600
    |||||||
Db 559 ctgcaccactaaagatgaccccaatgagcaataatcgaatgacatccacagatctac 618
QY 601 AAAGCACCAAGATGATTTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTTGTGA 660
    |||||||
Db 619 aaagcaccagaattgattcttgatatacaaatatgaatgaatgaatgaatgaatgaatga 678
QY 661 TTGGGTATATTTTGGTGTATATTCAGAAAATTTTCAAGGTGTTTACCAAGAT 720
    |||||||
Db 679 ttgggtataatttgactggttataatcagaataattccaagtgcttgaagcaagat 738
QY 721 GATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
    |||||||
Db 739 gataaagaattgactaatgattctcatgtaagattatattataataacaaatatt 798
QY 781 GAAATTTGCGTACCCCAATTAATGATGATTTTGAAGATGATTTTGTGATGAATAT 840
    |||||||
Db 799 gaaatttcgatacaaccaatttaactgatttgaagatgaatatttcttgatgaata 858
QY 841 AATAATGAAACCTTGCTTTTAAATAATCAATTTTCAAAAATATCTGAAAGATTTGG 900
    |||||||
Db 859 aataatgaaacttgcaattttaaaaaatccaatccaatccaatccaatccaatccaatcca 918
QY 901 GATATTTTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
    |||||||
Db 919 gatattatcttaactcgaatgcaatgattcattcaagaagaattttttccaagaatgatt 978
QY 961 AGATATGATGAGATTAAGATTAATCTTAAGAAATCTTACATTAATGATGATGATGATG 1019
    |||||||
Db 979 agatatgatcgaagttcaagaataacttcaagaagaatttcaactaactaactaactaactg 1037

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RESULT 13

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US-60-127-461-6643
; Sequence 6643, Application US/60127461
; GENERAL INFORMATION:
; APPLICANT: Chapman, Roman
; APPLICANT: Thornton, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANDIDA ALBICANS
; FILE REFERENCE: PM-0007-2 P
; CURRENT APPLICATION NUMBER: US/60/127,461
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 8247

```

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; SOFTWARE: PERL Program
; SEQ ID NO 6643
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: ATF808591841
US-60-127-461-6643

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Query Match          25.7%; Score 262; DB 51; Length 262;
Best Local Similarity 100.0%; Pred. No. 7.9e-34;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 492 TATAACACACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
    |||||||
Db 1 tataacacacagctattatgagatattgataattgtaattgtaattaaactgcacactaa 60
QY 552 AGATGACCCCTATGCGGAAATATATTGATGATGATGATGATGATGATGATGATGATGATGAT 611
    |||||||
Db 61 agatgaacccctatgcggaatatatgattgatactcaagctattataaagaccaga 120
QY 612 ATTGATTTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 671
    |||||||
Db 121 atgattcttggtataactaatatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 180
QY 672 TTTGACTGTTTATTAATTCAGAAAATTTTCAAGGTGTTTACTCAAGATGATGAATTAAGAT 731
    |||||||
Db 181 ttgacttggttataatccaagaatttccaagtgcttgaatgaatgaatgaatgaatgaatga 240
QY 732 GACTAATGATTTCTCATGTTACT 753
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Db 241 gactaatgattcctcatgtaagt 262

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RESULT 14

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US-60-127-461-3655
; Sequence 3655, Application US/60127461
; GENERAL INFORMATION:
; APPLICANT: Chapman, Roman
; APPLICANT: Thornton, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANDIDA ALBICANS
; FILE REFERENCE: PM-0007-2 P
; CURRENT APPLICATION NUMBER: US/60/127,461
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 8247
; SOFTWARE: PERL Program
; SEQ ID NO 3655
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2SY808579310
US-60-127-461-3655

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Query Match          25.6%; Score 260.4; DB 51; Length 262;
Best Local Similarity 99.6%; Pred. No. 1.5e-33;
Matches 261; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 606 ACCAAGATTTGATTTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTTGGTGGG 665
    |||||||
Db 1 accagaattgattcttgataactaatatgaataagaatgataattggtcattggg 60
QY 666 TATAATTTGACTGTTTATATTCAGAAAATTTTCAAGTGTGTTTACTCAAGATGATTA 725
    |||||||
Db 61 tataatttgactggtttataatccaagaatttccaagtgcttgaatgaatgaatgaatgaatga 120
QY 726 AGAATGACTAATGATTTCTCATGTTAGTATTTATTTATTTATTAATTAATTAATTTTGA 765
    |||||||
Db 121 agaattgactaatgattcctcatgtaagattatattataataataatattgaaaa 180
QY 766 TTTGCTACACCAATTAATGATTTTGAAGATGAATTAATTTGTTGATGAATTAATTA 845

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us-09-072-994a-13.rtf

Page 11

RESULT 15
US-60-127-461-6591
; Sequence 6591, Application US/60127461
; GENERAL INFORMATION:

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? TITLE OR INVENTION: NUCLEOTIDE SEQUENCES OF CANDIDA ALBICANS
?
? FILE REFERENCE: PM-0007-2 P
?
? CURRENT APPLICATION NUMBER: US/60/127,461
?
? CURRENT FILING DATE: 1999-04-01
?
? NUMBER OF SEQ ID NOS: 8247
?
? SOFTWARE: PERL Program
?
? SEQ ID NO 6591
?
? LENGTH: 260
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? FEATURE: -
?
? OTHER INFORMATION: ATE808591828
?
? OS-60-127-461-6591

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Query Match	25.3%;	Score 258;	DB 51;	length 260;
Best Local Similarity	100.0%;	Pred. No. 3.6e-33;		
Matches 258; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	492	TATTAACACAAACCGATTATTGAGATTGTAATTTGTATGATTTAAACTGACACTAA	551
Db	1	tataacaacacccgattattggaattttgatatttgcataactgacacctaa	60
QY	552	AGATGAAACCCCTATGCGCAATATATATGATATCTACAGGATTTATTAACACACAGA	611
Db	61	agaagaacccccctatggcgaatatattgattgctacagagatttataagcacaga	120
QY	612	ATTATCTCTTGCTATACATAATTATGAAATATGAAATGATATTGGTCATTGGGTATAT	671
Db	121	atgatctcttggtaactaactaattgaaatgaattgatacttggatcattggtataat	180
QY	672	TTTGACGTGTTATATTCAGAAATTTTCAAGGTTTACGCAAAAGATCATTAAGATT	731
Db	181	tttgacgtgttatattccagaanaatttccaagtgttttgctcaagaatgataaagaatt	240
QY	732	GACTAATGATTCATCTGT	749
Db	241	gactaatgattctcatgt	258

Search completed: May 29, 2002, 14:50:37
Job time: 17726 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:55:12 ; Search time 66.37 Seconds
(without alignments)
3771.290 Million cell updates/sec

Title: US-09-072-994A-13

Perfect score: 1019

Sequence: 1 AVGAGTTGTCAGATTATTA.....TTACATTAAATGTTGATWG 1019

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgcn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgcn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgcn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgcn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgcn2_6/ptodata/1/lna/PCRTUS.COMB.seq:*
6: /cgcn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.8	6.1	615	4	US-08-998-416-186
2	59.6	5.8	1431	4	US-09-316-083-2
3	59.4	5.8	828	4	US-08-998-416-538
4	59	5.8	834	4	US-08-998-416-305
5	58.6	5.8	665	2	US-08-883-795A-36
6	58.2	5.7	665	2	US-08-883-795A-36
7	58.2	5.7	19124	2	US-08-487-826B-13
8	57	5.6	636	4	US-08-998-416-1137
9	56.2	5.5	8920	2	US-08-446-855A-1
10	56.2	5.5	8920	4	US-09-150-741-1
11	54.4	5.3	767	4	US-08-998-416-472
12	53.8	5.3	724	4	US-08-998-416-683
13	53.8	5.3	854	4	US-08-998-416-534
14	53.8	5.3	860	4	US-08-998-416-287
15	53.6	5.3	837	4	US-08-998-416-288
16	53.4	5.2	663	4	US-08-998-416-191
17	53.4	5.2	19124	2	US-08-487-826B-13
18	53	5.2	1070	1	US-08-463-090B-5
19	52	5.1	837	4	US-08-998-416-288
20	51.8	5.1	51952	3	US-08-947-823-1
21	51.4	5.0	2483	1	US-08-526-964-1
22	51.4	5.0	2483	2	US-08-946-617-1
23	51.4	5.0	2483	3	US-09-031-897-1
24	51.4	5.0	5203	4	US-09-237-770-1
25	50.8	5.0	1431	4	US-09-316-083-2
26	50.6	5.0	615	4	US-08-998-416-186
27	50.6	5.0	724	4	US-08-998-416-683

C 28	50.6	5.0	6124	4	US-08-213-419B-3	Sequence 3, Appl1
C 29	50.4	4.9	711	4	US-08-998-416-786	Sequence 786, App
C 30	50.4	4.9	2317	3	US-08-749-512-5	Sequence 5, Appl1
C 31	50.4	4.9	3974	4	US-08-467-504-3	Sequence 3, Appl1
C 32	50.4	4.9	6124	4	US-08-213-419B-3	Sequence 1, Appl1
C 33	50.4	4.9	8920	2	US-08-446-855A-1	Sequence 1, Appl1
C 34	50.4	4.9	8920	4	US-09-150-741-1	Sequence 1, Appl1
C 35	50.2	4.9	662	4	US-08-998-416-185	Sequence 185, App
C 36	50.2	4.9	665	4	US-08-998-416-937	Sequence 937, App
C 37	50.2	4.9	732	4	US-08-998-416-1036	Sequence 1036, App
C 38	50	4.9	701	4	US-08-998-416-701	Sequence 701, App
C 39	50	4.9	854	4	US-08-998-416-534	Sequence 534, App
C 40	49	4.8	1511	1	US-07-991-867B-8	Sequence 8, Appl1
C 41	49	4.8	1511	1	US-08-107-755A-8	Sequence 8, Appl1
C 42	49	4.8	1511	2	US-08-544-332-8	Sequence 8, Appl1
C 43	48.8	4.8	636	4	US-08-998-416-1137	Sequence 1137, App
C 44	48.8	4.8	827	4	US-08-998-416-535	Sequence 535, App
C 45	48.8	4.8	1395	1	US-07-991-867B-25	Sequence 25, Appl1

ALIGNMENTS

RESULT 1
US-08-998-416-186/C
Sequence 186, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESS: NO. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NO. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: P61074RP


```

: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264rtis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 538:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 828 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1375RP
US-08-998-416-538

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Query Match          5.8%; Score 59.4; DB 4; Length 828;
Best Local Similarity 48.8%; Pred. No. 0.0063;
Matches 191; Conservative 0; Mismatches 196; Indels 4; Gaps 1;

QY 632 ATTATCAATATGAAATGATTTGGTCATTTGGTATTAATTTGACTGGTTATATTCAG 691
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 633

QY 692 AAAATTTCAAGTCTTAGTCAAAAGATGAATGAAGAAATTCCTATGATTCATGTTA 751
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 573

QY 752 GTGATTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 811
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 TTAATTTATATCTTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 513

QY 812 TTGAAGATCAATTTATTTTGTGATGA---ATATTAATGAAGAACTTGCAATTTAAAA 867
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 TAGGTAATTAATTTAGTAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 453

QY 868 TTCAATTTCAAAATATCTAGAAAAGATTTGGATATTATTTTCCGATGCAATGAT 927
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 TTACTAGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 393

QY 928 GATTTAATGAAGAAATTTTACCAAGATGATTAGATGATGCAAGTAAGAAATTAAT 987
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 392 GAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 333

QY 988 TCTAAGAAATCTTCAATTAATTTGATTT 1018
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 ATAACTATTTATTAATTAATTAATTTGATTT 302

```

```

RESULT 4
US-08-998-416-305/c
: Sequence 305, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Philippesen, Peter
: APPLICANT: Pohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christine
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtle, Philipp
: APPLICANT: Reblschung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264rtis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 305:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 834 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1250RP
US-08-998-416-305

```

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Query Match          5.8%; Score 59; DB 4; Length 834;
Best Local Similarity 48.8%; Pred. No. 0.00075;
Matches 190; Conservative 0; Mismatches 195; Indels 4; Gaps 1;

QY 634 TATGATATGAATTTGATTTGGTCATTTGGTATTAATTTGACTGGTTATATTCAGAA 693
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 689 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 630

QY 694 AATTTTCAAGTCTTAGTCAAAAGATGAATGAAGAAATTCCTATGATTCATGTTAGT 753
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 AATTAATTAATTAATTTAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 570

QY 754 GATTTATATTTATTAATTAATTAATTTGAAATTTTGGTACACCAATTTAATGATTTT 813
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 AATTAATTAATTTAGTAAATTAATTAATTTGATTTGATTTGATTTGATTTGATTT 510

QY 814 GAAGATGAATTTATTTTGTGATGA---ATATTAATTAAGAAACTTGCAATTTAAAAAT 869
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 GGTAAATATTTAGTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 450

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QY	870	CAATTTACAAAATATCTCTGAAAGATGGGATATATATTTACCTCGATGCATGTGA	929
Db	449	ACTGACGACATATATATATATATATATGTAAGGTGCATTATATATATATATCATGA	390
QY	930	TTTATATGAAAGAAATTTTACCAAGATGATAGTATATGATCGAGTAAAGAAATACCTC	989
Db	389	AGTAT	350
QY	990	TAAAGAAATCTTACATTAATGTGGATT	1018
Db	329	AATCTATTTATTAATATAAAAAGGATATATT	301

RESULT 5
 US-08-883-795A-36/C
 Sequence 36, Application US/08883795A
 Patent No. 5985607
 GENERAL INFORMATION:
 APPLICANT: Delcuvae, Genevieve
 APPLICANT: Awang, Gregor
 TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,795A
 FILING DATE: 27-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Michelle
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 7841-062
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Rh 32

	Query Match	5.8%;	Score 58.6;	DB 2;	Length 665;	
	Best Local Similarity	47.2%;	Pred. No. 0.00088;			
	Matches 178; Conservative	0;	Mismatches 199;	Indels 0;	Gaps 0;	
OY	15	TTATATTATAGCAAGAATTAATTACACATGTCGCATTTCTGTATATATACGGCTAT	74			
Dd	464	TTTAAATAATATGTAATTTAATAAATATGTAATATTAACAATTTTAATTTAATAATATGTAA	405			
OY	75	TGATATAGTTTAATTAACCTACCAGTAGTGCTCTTAAATAGTATGATGAAGTTCAGCTTCC	134			
Dd	404	TTTAAACCATTTTAATTAATTAATAATATGTAATATTAACAATTTTAATTTAATAAATATGTAA	345			
OY	135	ACCAATTCATCATTCAATCGAAGAAATTTTTTAAGTCTTGAAGACACATCCAAACAT	194			

Db	344	TTATTAACATTTTATTAATATAAAATATGTAATTATAAACATTTTAATTATAAAATATTTAA	285
Qy	195	AATGATATTTTATTTATGATCTTAATAATTTATGAGATGATATATATGTCACCAATTTGA	254
Db	284	TTATTAACATTTTATTAATATAAAATTTTAATTAATAATTTTAATTTAATTTAATAATTTAA	225
Qy	255	TGCTATGATTTGAGCAATTTGATTTGAATATTCAAATAATTTGTAAAGCAACACAGCAT	314
Db	224	TTATTAATATTTTATTAATATAAAATATTTAAATATAAAATATTTTAATTTAATAATTTTAA	165
Qy	315	TATTTATGCTATTTATGTTATCTTGTTAGTATCAATATCACTTGCTATGAAATTTGA	374
Db	164	TTATTAATATTTTATTAATATAAAATATTTAATTAATAAATTTTATTAATATAAAATATTTAA	105
Qy	375	AGAAAAAGATATCAAT	391
Db	104	TTATTAATATTTTAAATT	88

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RESULT      6
US-08-883-795A-36
; Sequence 36, Application US/08883795A
; Patent No. 5985607
;
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
;
; ZIP: M5H 3Y2
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Michelle
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
;
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: Rh 32
;
US-08-883-795A-36

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Query Match	5.78;	Score 58.2;	DB 2;	Length 665;
Best Local Similarity	46.8%;	Pred. No. 0.0011;		
Matches 254; Conservative	0;	Mismatches 283;	Indels 6;	Gaps 2;

OY 4 AAGTGTGAGATTATTATTAGACAAAGCATTAAATTACAAAGGCCATTTCGATATA 63

|||||

ADDRESS: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-08-998-416-287
 14
 ; Sequence 287, Application US/08998416
 ; Patent No. 639264
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Philippson, Peter
 ; APPLICANT: Pohlmann, Rainer
 ; APPLICANT: Steiner, Sabine
 ; APPLICANT: Moir, Christine
 ; APPLICANT: Wendland, Jürgen
 ; APPLICANT: Knechtle, Philipp
 ; APPLICANT: Reibtschung, Corinne

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OM protein - protein search, using sw model

Run on: May 29, 2002, 09:58:57 ; Search time 12.26 Seconds
(without alignments)
790.728 Million cell updates/sec

Title: US-09-072-994A-14

Perfect score: 1 WKLSDYIDKELIYNSAISD.....IRYDRSKRTSKETQLMD 339

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118494 seqs, 28596836 residues

Total number of hits satisfying chosen parameters: 118494

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/pdata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/pdata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/pdata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/pdata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/pdata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/pdata/2/paa/US60_NEW_COMB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	14.7	315	5	US-09-573-655B-294
2	262	14.6	298	7	US-60-366-892-7
3	256	14.3	305	7	US-60-366-892-8
4	255.5	14.3	424	7	US-60-366-892-39
5	253.5	14.2	236	5	US-09-863-776-40
6	249	13.9	292	7	US-60-370-796-7
7	240.5	13.4	297	7	US-60-366-892-6
8	236.5	13.2	427	7	US-60-366-892-38
9	235	13.1	360	7	US-60-366-892-43
10	235	13.1	426	5	US-09-909-650A-24
11	235	13.1	464	5	US-60-366-892-40
12	232	13.0	444	5	US-09-573-655B-1255
13	224.5	12.5	323	1	PCT-US02-13142-8265
14	224.5	12.5	323	6	US-10-128-714-3141
15	224.5	12.5	527	6	US-10-102-806-490
16	224	12.4	367	7	US-60-366-892-24
17	222.5	12.4	404	1	PCT-US02-13142-8141
18	222.5	12.4	404	6	US-10-128-714-8141
19	221.5	12.4	256	5	US-09-863-776-41
20	221.5	12.4	346	7	US-60-366-892-12
21	220	12.3	299	1	PCT-US02-13142-3141
22	220	12.3	299	6	US-10-128-714-3141
23	220	12.3	333	5	US-09-573-655B-1256
24	218	12.2	335	5	US-09-393-212-8
25	218	12.2	379	7	US-60-366-892-19
26	218	12.2	393	5	US-09-393-212-2

27	218	12.2	404	5	US-09-393-212-7	Sequence 7, Appl
28	216	12.1	815	7	US-60-366-892-23	Sequence 23, Appl
29	215	12.0	360	7	US-60-366-892-20	Sequence 20, Appl
30	215	12.0	380	5	US-09-393-212-9	Sequence 9, Appl
31	215	12.0	721	7	US-60-366-892-21	Sequence 21, Appl
32	213.5	11.9	464	7	US-60-366-892-13	Sequence 13, Appl
33	211.5	11.8	260	5	US-09-718-033-5	Sequence 5, Appl
34	209.5	11.7	268	1	PCT-US02-13142-3265	Sequence 3265, Ap
35	209.5	11.7	268	6	US-10-128-714-3265	Sequence 22, Appl
36	206	11.5	557	7	US-60-366-892-22	Sequence 22, Appl
37	206	11.5	586	5	US-09-393-212-10	Sequence 10, Appl
38	206	11.5	587	1	PCT-US02-10818-2	Sequence 2, Appl
39	204.5	11.4	1150	6	US-10-108-603-301	Sequence 301, App
40	203	11.3	292	7	US-60-366-892-10	Sequence 10, Appl
41	203	11.3	304	7	US-60-365-264-699	Sequence 699, App
42	202	11.3	465	7	US-60-365-264-370	Sequence 370, App
43	201	11.2	420	1	PCT-US02-13511-1	Sequence 1, Appl
44	201	11.2	420	6	US-10-135-255-1	Sequence 1, Appl
45	200.5	11.2	370	5	US-09-762-154-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-09-573-655B-294
Sequence 294, Application US/09573655B
GENERAL INFORMATION:
APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
FILE REFERENCE: 2750-0876P
CURRENT FILING DATE: 2000-05-18
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: Patentin version 3.0
SEQ ID NO 294
LENGTH: 315
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-573-655B-294

QY	11	ELIYSAISDIYTAIDFNNLPVCLK---IVDEDESLPHSHREITFIKTLKPHNIE	67	Sequence 294, Appl
DB	20	EKVGSGYGVYRAREKATGMVALKTRLHEDEGVPTTLREISILRLMARDPHYR	78	Sequence 8, Appl
QY	68	YFNDIK-----IYDYLVTKLYRYDLSQLIEITRYCKRTTFIYGINLVNQ	117	Sequence 39, Appl
DB	79	LM-DVKQINKREGTVLV---LVFEVDPDLKKFI-----RSFR-----	113	Sequence 40, Appl
QY	118	YTLAIEEKDKILKLSMSGSEFIHSOGIIRHDIKSIIFAPADINOPTIGDICY	177	Sequence 7, Appl
DB	114	-QAGNITQNTNKKLMQLCGMARFGHGYLRDLKPHMLMDRKTMLKLA-----	165	Sequence 8, Appl
QY	178	DKLPKDEPMAYIT-DVSTGIYKAPDLITGNVEYIDISGLITGLYSENFQSV	236	Sequence 8265, Ap
DB	166	DGLRLARATLLPMKRYTTEIILFWRAPEVLGATVSTGVDMVSCVIAELVTK--QAI	223	Sequence 8265, Ap
QY	227	LVKDQKELTNSHVSQDYLLNIOIFENGTFTNDFEDELPCDEYNNENLHFKFNLYQY	296	Sequence 24, Appl
DB	224	FAGD-----SELQILIRIRLIGTR-----EAVPGYSKLKDW-----EYF	261	Sequence 8141, Ap
QY	297	RKDW-----DILPRCNDLMLKEITFMIRYDSKRITSKILQ	335	Sequence 41, Appl
DB	262	Q--WKPLSLTAVPNL-DEAGIDLSKMLEYEPARKISAKKAME	302	Sequence 12, Appl
RESULT	2			

```

US-60-366-892-7
: Sequence 7 Application US/60366892
: GENERAL INFORMATION:
: APPLICANT: Prescott, John C.
: TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
: FILE REFERENCE: SUNEIS.006PR
: CURRENT APPLICATION NUMBER: US/60/366,892
: CURRENT FILING DATE: 2002-03-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-60-366-892-7

Query Match 14.6%; Score 262; DB 7; Length 298;
: Best Local Similarity 26.2%; Pred. No. 6,8e-10;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;

OY 21 IYTPIDKFNPLPYCLAIY--DEDFSLPHSHIREIFILTKTPHPNILEYENDLKIYDV 78
D 18 YKARNKLTGEVVALKRIKRLDTETEGVSTALREISLTKELN-HNNIYKILDIVITEKTL 76
OY 79 ILVTKLYRVDLSQLEITRYCKRTTRFYIYINGNLVSNQYTLANEIEEKDKIMLKSMS 138
D 77 YLVEEFLHODIKKFMDSA-----LTGIPLP-----IKSYLFOLLO 113
OY 139 GLEFTHSGIILHRIKPSNIFEFARDIHOPIITGDFDICYDLKLPKDEPPMAKYI-DVST 197
D 114 GLAFHSHRVLHRLDKLPQNLINTGALK--LADPGLARFQV-----PVITYTHEVYT 165
OY 198 GIYKAPDELITGTYEYEDIDWSIGILTGLYSENFQSVLYKDXELTNDSHVSDLYLIN 257
D 166 LMYRAPEILIGCKYYSFVADWISLCCIF-----AEMVTRALFPDSEIDOLF--- 213
OY 258 QIEENFGPNLTFDEDFELFCDEYNMNEHFFKFNLOKYPKRMIDILPCNDLKEIFPT 317
D 214 RIFRLTGTFPDEYVWGVVISMPTY-----KPSFPKARQDFSKVVPPLDED-GRSLIS 264
OY 318 KMIRYDRSKRRTISKEIL 334
D 265 QMLHYDPNKRISAKAAL 281

RESULT 3
US-60-366-892-8
: Sequence 8, Application US/60366892
: GENERAL INFORMATION:
: APPLICANT: Prescott, John C.
: TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
: FILE REFERENCE: SUNEIS.006PR
: CURRENT APPLICATION NUMBER: US/60/366,892
: CURRENT FILING DATE: 2002-03-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 305
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-60-366-892-8

Query Match 14.3%; Score 256; DB 7; Length 305;
: Best Local Similarity 25.8%; Pred. No. 1,6e-09;
Matches 87; Conservative 58; Mismatches 128; Indels 64; Gaps 12;

OY 5 IYIKELILYNSAIDVIAIDKFNPLPYCLAIYDEDFSLP--PHSHIREIFILTKLPKH 62
D 2 DMFQKVEKIGESGYGVVYAKNRRGQVALAKKIRLDLMEGVPSVAIREISLTKELK-H 60
OY 63 PNIEEYF---NDLKIYDVILVTKLYRVDLSQLEITRYCKRTTRFYIYINGNLVSNQY 118

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Db      61  PNIVRLDVLVHENERKLY-----LVFEFLSQDLKKWYDS*P----- 95
QY      119  TLVANIIEKDKIKIMKMSGSELEFHSOGIIRHDIKPSNIFEARRDITQPIIGEDICVD 178
Db      96  --GSLPRLHLKSYIFQLLQGVSRCHSRVIRHDIKPNLLI--NELGATKLADPGLARA 151
QY      179  LKLPRKDEPPAKRYI-DVSTGSIYKAPELLIGITWNEYEIDWISGIIITGLIXSENFOSVL 237
Db      152  FGV-----PIRTYTHEVVTLMYRAPELILGSKFETTVADWISGICIP-----AEM 196
QY      238  VKDKEKELINDSHVSDLYLLNLIQENFGPNITLDFEDELFCCEYNNENMLHFKFKNLQRYPR 297
Db      197  VTRKALPFGDSEIDOLF--RIFRMLGTPSSEDYWGCVIQLDPY-----KGSPPKNT 245
QY      298  KDWIILIPRCNDMLMKEITFTKIRYDRSKRITSKEIL 334
Db      246  KGLEIIVNLEPE-GRDILMQLLQYDPQSRITAKTAL 281

RESULT 4
US-60-366-892-39
; Sequence 39, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SURESIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 39
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-39

Query Match      14.3%; Score 255.5; DB 7; Length 424;
Best Local Similarity 27.1%; Pred. No. 2.6e-09;
Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps 16;

QY      21  IYTAIDKENNLPVCIKYDEDEFSLEPPHS--IHREIFILTKLPHRNIIEYEN-----DL 72
Db      40  YCAAEPTVLGISVAAKSLRSPONQTHAKRAARELVLLKCVN-HKNIISLWVTPQKTL 98
QY      73  KIYDVVITVTKLYRDLSQLIEITFKYCKRTFRFVIGINGNLVSNQYTLANEIEKDIKIM 132
Db      99  EEFQDITVLMEIADANLCOVIHM-----EIDHERMSYLL 131
QY      133  LKSMSSGSELEFHSOGIIRHDIKPSNIFEARRDITQPIIGEDFI---CYDLKLPRKDEPP 188
Db      132  LVQMLCGIKIHLHSAGIIRHDLKPSNT-VYKSCDTKLIL-DFGLARTACTNFMATPY---- 185
QY      189  MAKYIDVSGIYKAPELLIGITWNEYEIDWISGIIITGLIXSENFOSVYVKDKDELINDS 248
Db      186  -----VYTRYRRAPEVILGM-GYKENVDWISVGCIM-----GELVKGCVIFQGTD 229
QY      249  HVSDDLVLNLIQIENFETPNITLDFEDELFCDEYNNENMLHFKFKNLQRYPR-----KWD 301
Db      230  HLDQ--WAKVIEQLGTPS-AEFMKKLOQTVYRNVY-----NRRPYPPKIFPEELFPDW- 278
QY      302  IILP-----RCNDLMLKEITFKMIRYDRSKRITSKEIILQ 335
Db      279  IFPSESERDKIKTSQARDLLSKMLVILDPDKRISYDEALR 317

RESULT 5
US-09-863-776-40
; Sequence 40, Application US/09863776
; GENERAL INFORMATION:
; APPLICANT: Splytek, Kimberly A
; APPLICANT: Majumder, Kumud

```

```

; APPLICANT: Tchernev, Velizar T
; APPLICANT: Mishra, Vishnu
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Li, Li
; APPLICANT: Taupier, Raymond J
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-020
; CURRENT APPLICATION NUMBER: US/09/863,776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/206,679
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,688
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,829
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/207,748
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/207,798
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/208,263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/208,831
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/209,451
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/210,060
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/219,507
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/221,337
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/221,927
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/263,135
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,688
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,694
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/threonine protein kinase, catalytic domain
; OTHER INFORMATION: Consensus Sequence
US-09-863-776-40
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Query Match          14.2%; Score 253.5; DB 5; Length 256;
Best Local Similarity 27.1%; Pred. No. 1.9e-09;
Matches 91; Conservative 47; Mismatches 99; Indels 99; Gaps 16;
```

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QY 11 ELIYNSAIDYTAIDKFNPNVCLKIVDED--FSLPHSHIEIFLTKLRHPNIEY 68
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 EVLGAGAGKAYLARDOTGRLVAIKYIKKKKKRREILREIKLKL-DHPNIV-- 61

QY 69 FNDKIYDVLVTKLYRYDSQLEITKYCKRTTREFIYNGNLVSNQYTLANEIEKD 128
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 ----KLVDVEEDDKLYL-----VMEYCEGDLE-----DLKKR-----GRLSDE 99

QY 129 IKMLKSSSGLEFIHSOGIIRHDIKSNIFPFARDITOPTIGDFDICYDLKLPDDEP 188
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 100 ARFYARQTLIALEYIHSOGIIRHDLKPENILDSDGHVK--LADFG----- 143
```

```

QY 189 MAKYID-----VSTGIYKAPELLGITNEYEYDIWSLGIITGLYSENFQSVLVK 239
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 LAKQDSGGLTLTFVGTPEPMAPEVLG--KGGRKAVDIMSGLVILYELTIG--RPPFG 200

QY 240 DDKELTJDSHVSDLYLLNQIFENFGPNLTFDEDELFCDEYNENNLHFKKFNLOKYPKD 299
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 201 DDOLLA-----LFKKIGKPK-----PPPPPE 222

QY 300 WDLIPRCNDLMEIFTKMIRYDRSKRTSKELLQ 335
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 WK-ISPEAK-DLIRKLLVK-----DPEKRLTAEBALK 252
```

```

RESULT 6
US-60-370-796-7
; Sequence 7, Application US/60370796
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Helentjais, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion and Seed Set
; FILE REFERENCE: 1421P
; CURRENT APPLICATION NUMBER: US/60/370,796
; CURRENT FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Zea mays
US-60-370-796-7
```

```

Query Match          13.9%; Score 249; DB 7; Length 292;
Best Local Similarity 25.4%; Pred. No. 4.3e-09;
Matches 86; Conservative 58; Mismatches 129; Indels 66; Gaps 14;
```

```

QY 5 DYVIDKELIYSAISDIYTAIDKFNPNVCLK---YVDEDFSLPHSHIEIFLTKLRP 61
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 DQYEVKEIGSGTYGVYKGGDRITNETIALKRLQEDGVPSTAI-REISLKEMG- 59

QY 62 HPNIE-----YFNDKIYDVLVTKLYRYDSQLEITKYCKRTTREFIYNGNLVSNQ 117
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 HNTVRLQEVVHNDKCIY---LVFEYLDLDLK-----KHMSSYDF----- 97

QY 118 YTLANEIEKDIKMLKSSSGLEFIHSOGIIRHDIKSNIFE--ARDITOPTIGDFDIC 176
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 98 -----KMRIVKSFVQIILGIVACHSHRYLRDLKPKMLLDRNNLIK--LADFGIA 149

QY 177 YDLKLPDDEPPMAKYIDVSTGIYKAPELLGITNEYEYDIWSLGIITGLYSENFQSV 236
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 150 RAFGIPVRTFTH-----EVTLMYRAPEIILGARHSTPVDVMSVCIF-----AE 195

QY 237 LVKDKKELTJDSHVSDLYLLNQIFENFGTPTNLDFEDELFCDEYNENNLHFKKFNLOKYP 296
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 196 MVNQKALFPDSEIDELF--KIFRIIGTPKKEWPGVASLPDY-----KSTPPKP 244

QY 297 RKDWIILPRCNDLMEIFTKMIRYDRSKRTSKELLQ 335
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 245 PVDLATVYPTLEPSGI-DLISKMLRLDPSKRITARAALF 282
```

```

RESULT 7
US-60-366-892-6
; Sequence 6, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNESIS 006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-6
```

```
Query Match          13.4%; Score 240.5; DB 7; Length 297;
Best Local Similarity 25.4%; Pred. No. 1.5e-08;
Matches 85; Conservative 61; Mismatches 127; Indels 61; Gaps 14;
```

```
QY 7 YIDKELIYNSAIDYTAIDKFNMLPVCLK---IVDEDFSLPHSHREIFILTKLADHP 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4 YRKIEIGGCTGVYKGRHKTGTQYVAMKIRLESEEGVSTAI-REISLKLRL-HP 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 64 NIIEYNDKIYDD-VIIVTKLRYDLSQLEITKYCKRTTFIYINGNVLVNSQYTLAN 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 62 NIVS-LQDVLMODSRLYLFEFLSMDLKYLD-----STPGQY----- 99
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 123 EIEEKDIKLKSMSSGLEFIHSGIIRHDIRPSNIFARDDITPIIGDFICYDLKP 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 100 -MDSLVKGLVQILQGIYFCHSRVLRHDLKPQNLLI--DDKGTIKLADFGLARAFGI- 155
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 183 PKDEPPMAKTI-DVSTGTYKAPPELLIGITNYEYIDMSLGIILGLYSENFQSLVADD 241
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 156 ----PIRYVTHEVVTLMWRSPEVLGSARYSPVDIMSIGTFELAKV----- 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 242 KETLN-DSHVSDELINQIFENFGTGNLIDFEDELFCDEYNNENLHFKKFNLOKYPKDW 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 201 KPLFHGDSELDQLE---RIFRALGTPNNVEYVEESLDQYKKTFFPKWKGSLASHVKN-- 255
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DILLPRCNDLMEIFTKMIRYDRSKRTSKETL 334
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 256 -----LDENGDLILSKMLIYDPARKISGMAL 282
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 8
US-60-366-892-38
; Sequence 38, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNESIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-38
```

```
Query Match          13.2%; Score 236.5; DB 7; Length 427;
Best Local Similarity 24.5%; Pred. No. 3.9e-08;
Matches 91; Conservative 55; Mismatches 111; Indels 115; Gaps 17;
```

```
QY 14 YNSAISD-IYTAIDKFNMLP-----VCLITVDEDFSLPHS--I 49
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 YSVETIGSTFVLKRYQNLKPRISGAQIVCAAYDALIERNVAIKRLSRPFQNTAKRA 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 50 HREIFILTKLPHNIIIEYN-----DLKITVDVILYTKLYRDLSQLLEITKYCKRTT 103
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 YRELVLAKVCYN-HKNIIGLNVETPQKSLSEFQDVYIVMLMDANICQVQIM----- 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 104 RFIYINGNVLVNSQYTLANEIEEKDIKLKSMSSGLEFIHSGIIRHDIRPSNIFEAR 163
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 122 -----ELDERHMSYLLXQMCIGIKHLHSGIIRHDLKPSNI-VKVS 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 164 DITPIIGDFICYDLKPLPKDEPPMAKYIDVSTGTYKAPPELLIGITNYEYIDMSLGI 223
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
DB 162 DCTLIKID-----FGLARAGTSFMMTPY--VTRRYRADEVILGM-GYKENVDLMSVGC 213
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 224 ILGLYSENFQSLVADKDKELTNDSHVSDLYLNLQIFENFGTGNLIDFEDELFCDEYNE 283
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 214 IMGEMVCH-----KLTPGROVIDQM--NKVLEQLGTP-----CPFE----- 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 284 NLHFKKF-----NLQKYPKRW-----DITLP-----RCNDLKEIFTKMIRYD 323
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 249 ---MKLQPTVRYVENRPVYAGYSFEKLPDVLFPADSEHNLKASQARDLISKMLVID 305
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 324 RSKRTSKETLQ 335
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 306 ASKRISYDEALQ 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 9
US-60-366-892-43
; Sequence 43, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNESIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-43
```

```
Query Match          13.1%; Score 235; DB 7; Length 360;
Best Local Similarity 24.6%; Pred. No. 4e-08;
Matches 84; Conservative 66; Mismatches 127; Indels 64; Gaps 13;
```

```
QY 2 KLSVDYIDKELIYNSAIDYTAIDKFNMLPVCLKIVDEDFSLPHS--IHREIFILTKL 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 EYEPYONLSPVGSAGVSCAFDTKGLVAVAKKLSRPFOSILHAKRTYRELRLKHM 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 60 KHPNIIIEYN-----DLKITVDVILYTKLYRDLSQLLEITKYCKRTTFIYINGNL 113
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 79 K-HENVIGLIDLVETPARSLSEFNVDYIVTILMGADLNNVYK---CQKIT----- 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 114 VSNQYTLANEIEEKDIKLKSMSSGLEFIHSGIIRHDIRPSNIFARDDITPIIGDF 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 124 -----DHRVQPLIQLIRGLKTYIHSAIIRHDLKPSNL-AVNEDCEKLIL--- 167
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 174 DICYDLKPLPKDEPPMAKYIDVSTGTYKAPPELLIGITNYEYIDMSLGIILGLYSENF 233
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 168 ---DFGLARHTDDCMETGY--VATRWYRAPPEIMLMHMYNOTVDIWSVGCIM----- 213
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 234 QSVLVADKDELNDSHVSDLYLNLQIFENFGTGNLIDFEDELFCDEYNNENLHFKKFN 293
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 214 -AELLTGRTLFPGNDHIDQLKILRL--VGTPGA-----ELL-KKISSESARNYIOSLT 263
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 294 KYPRKDWIILPRCNDLMEIFTKMIRYDRSKRTSKETL 334
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 264 QMPKMFANVFIGAN-PLAVDLLEKMLVLDSDKRTITAAQAL 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 10
US-09-909-650A-24
; Sequence 24, Application US/09909650A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Fournier, Alain
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Deaunis-Cremond, Francine
; TITLE OF INVENTION: New Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CMT-1
```

```

CURRENT APPLICATION NUMBER: US/09/9309,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 426
TYPE: prt
ORGANISM: homo sapiens
US-09-909-650A-24

```

Query Match	13.1%;	Score 235;	DB 5;	Length 426;
Best Local Similarity	23.8%;	Pred. NO. 4.9e-08;		
Matches	91;	Conservative	62;	Mismatches 114;
				Indels 116;
				Gaps 18;

```

0Y 3 L50I11DCELL1NSA1SD-111ALDANNNL- - - - - VLCKIYDE 40
Db 1 M5SKVDNO- FYSVEG8STFVLKRRQNKPKIGSGAGIYCAAYDAVLDNRVAKIKLSR 59
0Y 41 DFLPAPHS-1IREF1ELKTKLPHNP1IEYFN- - - - - DUKIYDV1VTKLYRDELSOL 92
Db 60 PPONHAKARAVRELVLKCVN- HKNIISL1NF7QK1LEERQDY1VLMELMDANLCQY 118
0Y 93 IEITKCKKRTTF IYGINSLVSNQV1YLANDIEKD1K1MLKSMSSGCLFTHSGI1HRD 152
Db 119 IOM- - - - - ELDBERSY1LYOMCG1KHLHSAI1HRD 151
0Y 153 IRKSNIFPARDIOTPIIGDFICYDLKLPKDEPPAKY1DVSG1YKAPEL1G1TNY 212
Db 152 LKRSNI-VKXSOC1KI1D- - - - - FGLAR1AG1SFMMP1P- - - - - V1R1Y1RA1P1V1LGM- - - - - GY 202
0Y 213 EYE1DIWS1G1I1L1GLYSENFQSV1LVADKELTNDHSVSD1Y1LNO1FENF8TP1ULDEE 212
Db 203 KENVAD1WSVGC1M- - - - - GEMVRKH1LTPG8DY1DQ- - - - - WNKV1EOL1P- - - - - 244
0Y 273 DELFCGEYNNULMHFKKF- - - - - NLQY- - - - - PKRDWD1ILP- - - - - RCNDLDM 312
Db 245 - - - - - CEF- - - - - MKK1Q1P1V1RNV1ENR1K1P1YAG1LFPK1LFPD1SLFPADSEHNK1LKASQA 294
0Y 313 KE1FTK1M1R1D1SK1R1SKE1LQ 335
Db 295 RDL1SKM1V1D1PAK1R1SV1D1DLQ 317

```

```

RESULT 11
US-60-366-892-40
; Sequence 40, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNEIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-60-366-892-40

```

```

Query Match:          13 1%;   Score 235;   DB 7;   Length 464;
Best Local Similarity 23.8%;   Pred No. 5.4e-08;
Matches 91; Conservative 62; Mismatches 114; Indels 116; Gaps 18.
3 LSDYIDDKELIVSAISD-IYTAIDKFNINP-----VCLKIYDVE 40

```

```

Db      39  MSKSAVDNQ--FYSVEVGSGSTFTVLKRYQNLKPIGSGAGIYCAAVDAVLDBNVAIKKLSR   97
OY      41  DFLSLPSPH--LHREFFILKTLKPRHNIETRN-----DLKIYDYVILVTLKRYDLSQ   92
Db      98  PFQONQTAHRAVRELVLAKVCVN--HKNIIISLNVFTPOKTLSEFDVYLVMELMANICOV   156
OY      93  IETTYCAKRTTREFIYINGINLVNSNOYTLANEIEEKDIKVLKMSSSGGLFTHSGIHHI   152
Db     157  IQM-----ELDBHRSMSYLLXQMLCGIKHLHSGIHRD   189
OY     153  IKPSNIEFARDITQPIIGDFDICVDLKLPRKDEPPAKYUIDVSGIYKAEBELIGITNY   212
Db     190  LKPSNI--VYKSDCTKILID-----FGLARTAGTSFMTMTPY--VYTRYRAAEVLIGM--GY   240
OY     213  EYEIDIMSLGIIILGLYSENFQSVLVKDKDELINDSHVSDLYLLNQIFENFGTEPLDPE   272
Db     241  KENVDIWSVGCM-----GEMVRHKILFPGRIDQ-----WNKVIEJLGTP-----   282
OY     273  DELFQDEVNENNELHKKF-----NLOKY-----PRKDWIDILP-----RQNDLDM   312
Db     283  -----CPEF-----MKKIQPTVRNVENRPKATGLTFKLPDLSLFPADSEHNKLKASQA   332
OY     313  KEIPTKMTIRYDRSKRITSKEIIQ   335
Db     333  RDLISKMLVLIDPAKRISYVDALQ   355

RESULT 12
US-09-573-655B-1255
; Sequence 1255, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVIEV, Victor and TROUKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750--0876P
; CURRENT APPLICATION NUMBER: US/09/573,655B
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1255
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-1255

```

Query Match	13.0%;	Score 232;	DB 5;	Length 444;
Best Local Similarity	23.0%;	Pred. No. 7.9e-08;		
Matches	80;	Conservative	60;	Mismatches 124;
			Indels	84;
			Gaps	12;

```

0Y 5 DYIDKELVNSAISDIYTAIDKPFNNLLPVCJAKYIVEDESLPASHIHFREIFILKTJAKPHN 64
   | : : : : | : : : : | : : : : | : : : : |
Db 131 DYEVAWR -VGRKXSEVEGEGIHATNEKCIVKILK---PVKKKKIKREIKLIONCGSPN 186
   | : : : : | : : : : | : : : : | : : : : |
0Y 65 IIEFYNDLKIYDDVLLVTKIKRYDLSQJLEITK -YCKRTFRIFYGINSVSNQ--YTLA 121
   | : : : : | : : : : | : : : : | : : : : |
Db 187 IV-----KLUDDYRDOQSFTPSLIF---EHWNNDEKVLV 218
   | : : : : | : : : : | : : : : | : : : : |
0Y 122 NEIEEKDIKLMWLSKSSGLEFIHSOGIITHRIDKPSNIEFARDIOTPIGDFIDICYDUL 181
   | : : : : | : : : : | : : : : | : : : : |
Db 219 PTLSDYDVRYYYIFELKLKLDFFCHSRGIMHRYVKPHNVMIDHQRKLRLL-----DWGL 271
   | : : : : | : : : : | : : : : | : : : : |
0Y 182 PKDEBPMAKYIDVETGTGYIKAPELLITGTYEYEDIMSLTGILGL-----YSENF 233
   | : : : : | : : : : | : : : : | : : : : |
Db 272 AEFYHPRGKEYNNRVASRRFKPGBELVDLODYISLDWLSGCMFAGMIFRKEPFYGGDN 331
   | : : : : | : : : : | : : : : | : : : : |
0Y 234 QSVLYAKDDKELTNDHSVSDYLJNQIFENFG--TPNLTDFEDELFCDEYNNENIMHFKKF 290
   | : : : : | : : : : | : : : : | : : : : |
Db 332 YDOLVKIKAVIGTDE-----LNAJLNYKRYRELDPPNNLST----- 365
   | : : : : | : : : : | : : : : | : : : : |
0Y 291 NLQKYPKRDWDIILPRCNDUL-----MKELFTKMIKYDSKRITTSKEIL 334
   | : : : : | : : : : | : : : : | : : : : |

```


; NAME/KEY: SITE
; LOCATION: (311)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-490

Query Match 12.5%; Score 224.5; DB 6; Length 527;
Best Local Similarity 24.1%; Pred. No. 2.8e-07;
Matches 81; Conservative 63; Mismatches 127; Indels 65; Gaps 13;

QY 7 YIDKELIYNSAISDIYTAIDKFNNTLPCVKIY--DEDESLPPSHIREIFILTKRPHN 64
|| :
Db 136 YIKDKLGEQIYAVYKSKLNDNLVALKEIRLHEHEGAPCTAI-REVSILKDLK-HAN 253
|| :
QY 65 IIEYFNDIKIYDDVILVTKLIRYDLSQLIEITKYCKRTTRFIYGINGLVSNQYTLANEI 124
|| :
Db 254 IVTLHDIHTEKSLTVEYLDKDLKQYLD-----DCGNTI 289
|| :
QY 125 EEKDIKIMLKSMSSGLEFISQGIHRDIKPSNIF-ARDDITQPIIGPEDICYDLKLP 183
|| :
Db 290 NMHWKLFELQILGLAYCHRXKYLHDLKPNLLINERGLK---LADGLARAKSIPT 346
|| :
QY 184 KDEPPMAKIYDVSTGIYKAPELLGITNVEYEDIMSLGILL---TGYSNFGSVLVK 239
|| :
Db 347 KTYSN----EYVTLWYRPPDILGSTDYSTQIDMWGVCIFYEMATG----- 389
|| :
QY 240 DDKELTNDSHYSGLYLNQIFENFGTPNLDFEDELFCDEYNENLHFKKFNLOXXPRD 299
|| :
Db 390 --RPLFPGSTIVEE--QLHFIIRIIGTPT---ETWPGILSNE--EFKTYNPKYRAEA 438
|| :
QY 300 WDIILPRCNDLIMKEIFTKMIYDRSKRITSKEILQ 335
|| :
Db 439 ILSHAPRLDSD-GADLLTKLLQFEGRRNRISAEDAMK 473
|| :

Search completed: May 29, 2002, 10:02:32
Job time: 215 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 29, 2002, 09:55:26 ; Search time 13.07 Seconds
(without alignments)
633.533 Million cell updates/sec

Title: US-09-072-994A-14

Perfect score: 1 MKLSYIDKELIYNSAISD.....IRYDRSKRITSKELIQLMD 339

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/prodata/2/1aa/backfilist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263.5	14.7	416	3 US-08-554-385-21	Sequence 21, Appl
2	262	14.6	391	4 US-09-131-028A-4	Sequence 4, Appl
3	262	14.6	391	4 US-09-131-028A-14	Sequence 14, Appl
4	261	14.6	298	2 US-08-874-347-25	Sequence 25, Appl
5	261	14.6	298	2 US-08-869-106-2	Sequence 2, Appl
6	261	14.6	298	2 US-09-093-522-25	Sequence 25, Appl
7	258.5	14.4	294	2 US-08-874-347-26	Sequence 26, Appl
8	258.5	14.4	294	2 US-09-093-522-26	Sequence 26, Appl
9	255.5	14.3	297	2 US-08-874-347-22	Sequence 22, Appl
10	255.5	14.3	297	2 US-09-093-522-22	Sequence 22, Appl
11	255.5	14.3	382	4 US-09-025-580-29	Sequence 29, Appl
12	255.5	14.3	424	3 US-09-209-668-17	Sequence 17, Appl
13	255.5	14.3	424	5 PCT-US94-12913A-18	Sequence 18, Appl
14	254.5	14.2	424	4 US-09-025-580-32	Sequence 32, Appl
15	252.5	14.1	365	4 US-09-025-580-27	Sequence 27, Appl
16	251.5	14.0	365	4 US-08-674-612-2	Sequence 2, Appl
17	251.5	14.0	365	2 US-08-920-296-2	Sequence 2, Appl
18	251.5	14.0	365	4 US-09-124-163-2	Sequence 35, Appl
19	248.5	13.9	384	4 US-09-025-580-35	Sequence 35, Appl
20	248.5	13.9	427	4 US-09-025-580-36	Sequence 36, Appl
21	247.5	13.8	382	4 US-09-025-580-30	Sequence 30, Appl
22	247.5	13.8	424	4 US-09-025-580-31	Sequence 31, Appl
23	246.5	13.8	365	2 US-08-746-788-2	Sequence 2, Appl
24	246.5	13.8	365	2 US-09-189-602-2	Sequence 26, Appl
25	246.5	13.8	365	4 US-09-025-580-26	Sequence 9, Appl
26	246	13.7	317	1 US-08-463-090B-9	Sequence 18, Appl
27	246	13.7	317	2 US-08-874-347-18	

28	246	13.7	317	3 US-09-093-522-18	Sequence 18, Appl
29	243.5	13.6	375	2 US-08-837-593-5	Sequence 5, Appl
30	243	13.6	360	3 US-08-554-385-20	Sequence 20, Appl
31	243	13.6	387	2 US-08-837-593-4	Sequence 4, Appl
32	241	13.5	371	2 US-08-837-593-6	Sequence 6, Appl
33	240.5	13.4	297	2 US-08-874-347-24	Sequence 24, Appl
34	240.5	13.4	297	2 US-09-093-522-24	Sequence 24, Appl
35	238.5	13.3	297	2 US-08-874-347-23	Sequence 23, Appl
36	238.5	13.3	297	2 US-09-093-522-23	Sequence 23, Appl
37	237.5	13.3	297	1 US-08-176-620A-16	Sequence 16, Appl
38	237.5	13.3	297	2 US-08-461-985-16	Sequence 16, Appl
39	237	13.2	370	2 US-08-837-593-7	Sequence 7, Appl
40	237	13.2	422	4 US-09-025-580-3	Sequence 3, Appl
41	236.5	13.2	353	1 US-08-176-620A-14	Sequence 14, Appl
42	236.5	13.2	333	2 US-08-461-985-14	Sequence 14, Appl
43	236.5	13.2	384	3 US-09-209-668-15	Sequence 15, Appl
44	236.5	13.2	384	4 US-09-025-580-33	Sequence 33, Appl
45	236.5	13.2	384	5 PCT-US94-08119-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-554-385-21
: Sequence 21, Application US/08554385
: Patent No. 6017692
: GENERAL INFORMATION:
: APPLICANT: Roger Brent
: APPLICANT: Antonis S. Zervos
: TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
: TITLE OF INVENTION: MOLECULES AND METHODS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM PS/2 Model 502 or 555X
: OPERATING SYSTEM: MS-DOS (Version 5.0)
: SOFTWARE: WordPerfect (Version 5.1)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/554,385
: FILING DATE: No. 6017692member 8, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Karen F. Lech
: REGISTRATION NUMBER: 35,238
: REFERENCE/DOCKET NUMBER: 00786/252001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200134
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 416 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-554-385-21
Query Match 14.7%; Score 263.5; DB 3; Length 416;
Best Local Similarity 23.7%; Pred. No 7.7e-16;
Matches 86; Conservative 66; Mismatches 98; Indels 113; Gaps 14;

APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-347-25

Query Match 14.6%; Score 261; DB 2; Length 298;
Best Local Similarity 26.2%; Pred. No. 8.2e-16;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;
QY 21 IYTAIDKNNLPVCLKIV--DEDSLPHSHHREIFLTKLKHPRNIEFNDKLYDOV 78
DB 18 YKANRKNLTGEVVALKRIKIDTETEGVSTAIRISILKELN--HPNIVKLLDVITHENKL 76
QY 79 ILVTKLYRVDLSQLEITKYCKRTTRPIYGINGNLVSNQYTLANEIEEKDIKLMKSMGS 138
DB 77 YLVEFELHQDLKRFMDASA-----LTGIPPL-----IKSYLFQLLQ 113
QY 139 GLEFHSOGIITHROIKNSNIFFARDITOPRIDFCIDYDKLPKDEPPMAKTI--DVST 197
DB 114 GLAFCHSHRVHLRDLKPNLINTGAIK--LADFGIARAFV-----PVRTYTHEVVT 165
QY 198 GIYKAPELLIGITNVEYEDIMSLGILTLGLYSENFQSVLVKDKKELTNDSHVSDLYLNL 257
DB 166 LMYRNPPELLLSKYSTAVDIMSIGCIF-----AEWVTRRALFPGDSEIDQLF--- 213
QY 258 QIFENFGPNLTDEDELFCDEYNNENLHKRKNLQKYPKKMDIILPRCNDLMKEIFT 317
DB 214 RIFRTLTGPDEYVMPGYTSMEDY-----KPSFPMARODESKVVPPLDED--GRSLLS 264
QY 318 KIRYDRSKRITSKEIL 334
DB 265 QMLHYDPKRIKISAKAL 281

RESULT 5
US-08-969-106-2
; Sequence 2, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.

APPLICANT: Nandabalan, K.
TITLE OF INVENTION: SCHULZ, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-969-106-2

Query Match 14.6%; Score 261; DB 2; Length 298;
Best Local Similarity 26.2%; Pred. No. 8.2e-16;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;
QY 21 IYTAIDKNNLPVCLKIV--DEDSLPHSHHREIFLTKLKHPRNIEFNDKLYDOV 78
DB 18 YKANRKNLTGEVVALKRIKIDTETEGVSTAIRISILKELN--HPNIVKLLDVITHENKL 76
QY 79 ILVTKLYRVDLSQLEITKYCKRTTRPIYGINGNLVSNQYTLANEIEEKDIKLMKSMGS 138
DB 77 YLVEFELHQDLKRFMDASA-----LTGIPPL-----IKSYLFQLLQ 113
QY 139 GLEFHSOGIITHROIKNSNIFFARDITOPRIDFCIDYDKLPKDEPPMAKTI--DVST 197
DB 114 GLAFCHSHRVHLRDLKPNLINTGAIK--LADFGIARAFV-----PVRTYTHEVVT 165
QY 198 GIYKAPELLIGITNVEYEDIMSLGILTLGLYSENFQSVLVKDKKELTNDSHVSDLYLNL 257
DB 166 LMYRNPPELLLSKYSTAVDIMSIGCIF-----AEWVTRRALFPGDSEIDQLF--- 213
QY 258 QIFENFGPNLTDEDELFCDEYNNENLHKRKNLQKYPKKMDIILPRCNDLMKEIFT 317
DB 214 RIFRTLTGPDEYVMPGYTSMEDY-----KPSFPMARODESKVVPPLDED--GRSLLS 264
QY 318 KIRYDRSKRITSKEIL 334
DB 265 QMLHYDPKRIKISAKAL 281

RESULT 6
US-09-093-522-25
; Sequence 25, Application US/09093522
; Patent No. 6015700
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.

APPLICANT: Leo F. Edward B.
 APPLICANT: Thomas, Charles F.
 APPLICANT: Gustafson, Michael P.
 TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
 TITLE OF INVENTION: CARINI
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C., P.A.
 STREET: 60 South Sixth Street, Suite 3300
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fastseq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/093,522
 FILING DATE: 08-JUN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/874,347
 FILING DATE: 13-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ellinger, Mark S.
 REGISTRATION NUMBER: 34,812
 REFERENCE/DOCKET NUMBER: 07039/055002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-335-5070
 TELEFAX: 612-288-9696
 TELEX:
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 298 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-09-093-522-25

Query Match	14.68;	Score 261;	DB 3;	Length 298;
Best Local Similarity	26.28;	Pred. No. 8.2e-16;		
Matches	83;	Conservative	59;	Mismatches 119;
			Indels	56;
			Gaps	11;

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OY 21 IYTAIDKENMLPVCLAKIV--DEDSLPHSIHREIFILKLTLPKPHNIIEXFNOLKIIYDV 78
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 VYKARNKLTGGEVVALKIRIDTETEGVSTAIRISLKEILN--HPNIVKLLVDIYHNENKL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 79 ILVVKLYAYDELSOLIEITKVCKRTRFRFYINGNLVSNQYTLANEIEEKDIKLMLKSMSS 138
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 YLVPEELHODLKKFENDASA-----LTGIPLEP-----IKSLFOLLQ 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 139 GLEFIHSOGILHRDKISNIFPFARDITOPITIGDFIDICYDLKLPKDEPPMAKY--DVST 197
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 GLAFCHSHRYLHRDLKPKQNLILINEGAIRK--LADFGLARAFGV-----PVRTYTHEVYT 165
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 198 GIYKAPELLIGITVXEYEDIWISUGIILTGLISENFOSVLYKKDELTLNDSHVSDLYLNL 257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 LMYRAPEITLISKYSTVAIVIMSLGCTF-----AEMVTRALPEPGSEIDOLF-- 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 258 OIFENFGPPNLTDEDELFCEDEYNNENLHKKFNLOKYPKRDWIIILPRCDDLMKELTF 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 RIFRTLGPDEVEVMPGVGVSMPDY-----KPSFPKWARODFSKVVPPLED--GRSLIS 264
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 318 KMIRYDRSKRITSKEIL 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 265 OMLHYDPNKRISAKAAL 281
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RESULT 7

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US-08-874-347-26
; Sequence 26, Application us/08874347
; Patent No. 5863741
;
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; TITLE OF INVENTION: CARINI I
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874.347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-874-347-26
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Query Match	14.4%;	Score 258.5;	DB 2;	Length 294;
Best Local Similarity	25.3%;	Pred. No. 1.4e-15;		
Matches	85;	Conservative	60;	Mismatches 132;
				Indels 59;
				Gaps 12;

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QY      5 DYIDKELIYSAISDIYTALDKENNNLPVCK-----LYDEDESILPRPHSHIEFIKLTKRP 61
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      2 EOYEKEERKIGEGTGVVARYADKVTNETIAKKIRLBOEDEGVSTAI-REISLSLEMH- 59
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      62 HNNIIEYNNDKIYDDVLVLTAKLYRYDLSOLIE-IITYCYKRRTFRFYGINGNLVSNOYTL 120
        ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      60 HGNIYRLHDVHSEKRITLVEYIEDLDLDTKKWDCSPFEAKPPL-----103
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      121 ANEIKEDIKLIMKSMSSGLEEFISHOGIHRDIPSNIFEARDDITOP I-TGDFICYDL 179
        || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      104 -----IKSLVGIOILNGVAACHSHRHLNDRMLPQNLLI--DRTNAKLADPGLARAF 153
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      180 KLPPKDPBPMAKYIVDSYGVIKABELIGITNYEYEDIMSGLIITGLYSNFOSVLYK 239
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      154 GIVPVTFTH-----EVVALWRAPRIILGSROYSGPYMDMWSVCIF-----AEMVN 189
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      240 DDKELLTNSHVSVDLYLLOEIFENFGSPMLPDFEBDELFCODEYNENNENLFFKFNLOKRYRKD 299
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      200 OKPLPCSCSEIDELF---KIRFVLGTBPMOSMPGVSSLDPY-----KSAPFKWAOD 248
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      300 WDIIILRCNDMLMKEIFTKMIHYRSKRKITSKELIO 335
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      249 LATIVPTL-DPAGIDILSRMKRYTENPKKITTIRAOALE 283
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Db 209 LPPGSEIDEIF---KIFQVLTGPNNEEVPQVTLIDQYKSTFPPRKRMDLHK----- 257

Qy 303 ILPRCNDLMKEIFTKMIRYDRSKRTSKETIQ 335
Db 258 VVPNGEEDAI-ELLSAMLVYDPAHRISAKRALQ 289

RESULT 10
US-09-093-522-22

; Sequence 22, Application US/09093522
; Patent No. 6015700
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 south sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093.522
; FILING DATE: 08-JUN-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/874,347
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-093-522-22

Query Match 14.3%; Score 255.5; DB 3; Length 297;
Best Local Similarity 24.3%; Pred. No. 2.6e-15;
Matches 81; Conservative 70; Mismatches 131; Indels 51; Gaps 11;

Qy 7 YIDKEILYSAISDIYTAIDKFNMLPYCLK---IYDEDESLPPHSHREIFLTKLKPMP 63
Db 4 YORVENKIGETYGAVVYKARHKLSGRIYAMKTKIRLEDESEGVSTAL-REISLKEVNDEN 62
Qy 64 NIEFYNDKIYDVILVTIKLYRYDLSQLEITKYCKRTTRFIYINGNMLVSNQYTLANE 123
Db 63 N---RSCNCRLLDILHAESKLVYFEFLMDLKKYMDRISE-----TGATS 105
Qy 124 IEKDKILMKSMSSGLEFIHSGIITHRIDKPSNIFPARDITQPIIGFDICYDLKLP 183
Db 106 LDRVLQKFTYQVLVNGVNCFSRRIIHRDLKPNLLIDKGNLK--LADFGIARSGV-- 161

Qy 184 KDEPPAKYI-DVSTGIYKAPPELLIGITNYEVEIDIMSLGIIITGLYSENFQSVLVKDK 242
Db 162 ----PLRNTYHELVTLMYRAPEVLGSRHYSVGDIWVGCF-----AEKIRSP 208

Qy 243 ELINDSVSDYLLYLNQIFENFETPNLTDEDELFCEYNNENLHFKKFMLOKYPKRDWI 302
Db 209 LPPGSEIDEIF---KIFQVLTGPNNEEVPQVTLIDQYKSTFPPRKRMDLHK----- 257

Qy 303 ILPRCNDLMKEIFTKMIRYDRSKRTSKETIQ 335
Db 258 VVPNGEEDAI-ELLSAMLVYDPAHRISAKRALQ 289

RESULT 11

US-09-025-580-29
; Sequence 29, Application US/09025580
; Patent No. 6162613
; GENERAL INFORMATION:
; APPLICANT: Su, Michael Shin-San
; APPLICANT: Fox, Ted
; APPLICANT: Wilson, Keith Phillip
; APPLICANT: Gorman, Ursula A.
; TITLE OF INVENTION: Methods For Designing Inhibitors of
; TITLE OF INVENTION: Serine/Threonine Kinases and Tyrosine Kinase
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025.580
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: VPI 97-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-580-29

Query Match 14.3%; Score 255.5; DB 4; Length 382;
Best Local Similarity 27.1%; Pred. No. 3.6e-15;
Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps 16;

Qy 21 IYTAIDKFNMLPYCLKIYDEDESLPPHS--IHREIFLTKLKPMPNITIEFN-----DL 72
Db 40 VCAAPFDIVLGISAVVAKLSRPFQNHAKRAVRELVLLKCVN-HKNILSLNVFTQKTL 98
Qy 73 KIYDVILVTIKLYRYDLSQLEITKYCKRTTRFIYINGNMLVSNQYTLANEIEKDKIM 132
Db 99 EEPQDVILVMEIAMDANLCQYIHM-----ELDHERSYL 131
Qy 133 LKSMSSGLEFIHSGIITHRIDKPSNIFPARDITQPIIGFDI---CYDLKLPKRDPP 188
Db 132 LYQMLCGIKHLSAGIITHRIDKPSNI-VKRSDCITLIL-DFGIARACTNFMMPY---- 185

APPLICANT: Su, Michael Shin-san
APPLICANT: Fox, Ted
APPLICANT: Wilson, Keith Phillip
APPLICANT: German, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
TITLE OF INVENTION: Serine/Threonine Kinases and Tyrosine Kinase
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-580-32

Query Match 14.28; Score 254.5; DB 4; Length 424;
Best Local Similarity 27.18; Pred. No. 5.1e-15;
Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps 16;
21 IYAIIDKFNMLPYCLKIVDEDFSLPPHS--IHRIFILTKLPHPNIIIEFN-----DL 72
40 VCAAFDVLGINAVAKLSRPQONQHAQKRAYRELVLKCVN-HKNIIISLVNFTPOKTL 98
73 KIYDVLVTKLYRYDLSQLEITKYCKRTTRFIYINGNLVSNQYTLANEIEKDIKIM 132
99 EEFQDVLVLMELMDANLCQVIM-----ELDHERMSYL 131
133 LKSSSGLEFIHSGIIRHRIKPSNIFFARDITOPITIGDFI-----CYDLKLPDEPP 188
132 LYQMLGSIKIHSAAGIIRHDLKPSNI-VKASDCTKLTL-DFGLARACTNFMATPY----- 185
189 MAKYIDVSTGIYKAPELLIGITNYEVEIDIMSGIILTGLYSENFOSVLVKDDKEILTND 248
186 -----VTRIRYRAPETILDM-GYKENVDIMSGCIM-----GEIVKGCVIFQGD 229
249 HVSDDLILNQLFENFGPNLTDPEDELFCDEYNENNLHFKFNLOKPYR-----KDM 301
230 HIDD-----WNVYIEOLGTPS-AEFKRLQPVYRNVE-----NPKYPIKFEELPPDW 278
302 IILP-----RCNDLMLKEIFTKMIRYDRSKRITSKEILQ 335
279 -IFPSESRDKITSQARDLKMLVLDPKRISVDEALR 317

RESULT 15
US-09-025-580-27
Sequence 27, Application US/09025580
Patent No. 6162613

GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-san
APPLICANT: Fox, Ted
APPLICANT: Wilson, Keith Phillip
APPLICANT: German, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
TITLE OF INVENTION: Serine/Threonine Kinases and Tyrosine Kinase
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-580-27

Query Match 14.18; Score 252.5; DB 4; Length 365;
Best Local Similarity 26.18; Pred. No. 6.3e-15;
Matches 90; Conservative 57; Mismatches 125; Indels 73; Gaps 14;
2 KISDYIDKELLVNSAISDIYTAIDKRNMLPYCLKIYDEDF--SLPSSHIREIFITKL 59
20 ELPKTYVSPFTVHSGAVSVCASIDKRSGEKVATIKLSRPFQSEIFAKRAYRELLIKHM 79
60 KPHPII---EYF--NDLKIYDVLVTKLYRYDLSQLEITKYCKRTTRFIYINGNL 113
80 Q-HENVIGLIDVETFPASSLRNFYDFILVMPMOTDLOKI----- 117
114 VSNQYTLANEIEKDIKIMLSKSSGLEFIHSGIIRHRIKPSNIFFARDITOPITIGDF 173
118 -----MGMEFSEKTIQVLVYOMLKLKYIHSAQVHRDLKPNL-AVNEDCEIKTL--- 167
174 DICYDIKLPKDEPMMAKIIDVSTGIYKAPELLIGITNYEVEIDIMSGIIL-GLY 229
168 -----DFGLARHADAMETG--VTRIRYRAPETILDSMWHYNOTVIDIMSGCIMAEMLTG-- 219
230 SENFOSVLVKDDKEILTNDSSHVDLYLNLQIFENFGPNLTDPEDELFCDEYNENNLHFK 289
220 -----KTLFKGKOYIDQ-----LVQILKYTCVPG-TFVQKL-----NDAKAS 259
290 FNLOKPYPRKMDIILPCNDLMLKEIFTKMIRYDRSKRITSKEIL 334
260 GSLPQTPRKDFTLQLPFRASPQ-AADLLKMLLELDVDRKRLTAQAOL 303

Search completed: May 29, 2002, 10:00:16
Job time: 290 sec

